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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) **International Patent Classification:** **C12N 15/12, A61K 38/39, A61L 31/00, A61P 9/00, A61P 21/00, A61P 25/00, C07K 14/78, C12N 5/10, C12N 15/62**

A2

(11) **International Publication Number:** **WO 00/66730**

(43) **International Publication Date:** 09 November 2000 (09.11.2000)

(21) **International Application Number:** PCT/US00/11378

(22) **International Filing Date:** 28 April 2000 (28.04.2000)

(30) **Priority Data:**

60/131,720	30 April 1999 (30.04.1999) US
60/139,198	15 June 1999 (15.06.1999) US
60/143,289	12 July 1999 (12.07.1999) US
60/155,945	24 September 1999 (24.09.1999) US

(60) **Parent Application or Grant**
UNIVERSITY OF MEDICINE AND DENTISTRY OF NEW JERSEY ROBERT WOOD JOHNSON MEDICAL SCHOOL [/]; (). YURCHENCO, Peter [/]; (). YURCHENCO, Peter [/]; (). HARPER, David, S. ; ().

Published

(54) **Title: LAMININ 2 AND METHODS FOR ITS USE**

(54) **Titre: LAMININE 2 ET SES METHODES D'UTILISATION**

(57) Abstract

The present invention provides substantially purified laminin 2, methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using the substantially purified laminin 2 to accelerate peripheral nervous system nerve regeneration, and to promote cell attachment and migration.

(57) Abrégé

La présente invention concerne une laminine 2 sensiblement purifiée, des méthodes de construction d'une laminine 2 de recombinaison, des cellules exprimant ladite laminine 2 de recombinaison, ainsi que des méthodes d'utilisation de la laminine 2 sensiblement purifiée visant à accélérer la régénération des nerfs du système nerveux périphérique et à favoriser la fixation et la migration cellulaires.

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(51) International Patent Classification 7 :
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60/143,289	12 July 1999 (12.07.99)	US
60/155,945	24 September 1999 (24.09.99)	US

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(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published

Without international search report and to be republished upon receipt of that report.

(54) Title: LAMININ 2 AND METHODS FOR ITS USE

(57) Abstract

The present invention provides substantially purified laminin 2, methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using the substantially purified laminin 2 to accelerate peripheral nervous system nerve regeneration, and to promote cell attachment and migration.

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Description

LAMININ 2 AND METHODS FOR ITS USE

Cross Reference

This application claims priority to U.S. Provisional Patent Application Serial Nos. 60/131,720 filed April 30, 1999; 60/139,198 filed June 15, 1999; and 60/143,289 filed July 12, 1999; 60/155,945 filed September 24, 1999; all of which are incorporated herein by reference in their entirety.

Field of the Invention

This application relates to recombinant laminin 5 and methods for its use.

Background of the Invention

Basal laminae (basement membranes) are sheet-like, cell-associated extracellular matrices that play a central role in cell growth, tissue development, and tissue maintenance. They are present in virtually all tissues, and appear in the earliest stages of embryonic development.

Basal laminae are central to a variety of architectural and cell-interactive functions (See for example, Malinda and Kleinman, Int. J. Biochem. Cell Biol. 28:957-959 (1996); Aumailley and Krieg, J. Invest. Dermatology 106:209-214 (1996)). For example:

1. They serve as architectural supports for tissues, providing adhesive substrata for cells.
2. They create perm-selective barriers between tissue compartments that impede the migration of cells and passively regulate the exchange of macromolecules. These properties are illustrated by the kidney glomerular basement membrane, which functions as an important filtration structure, creating an effective blood-tissue barrier that is not permeable to most proteins and cells.
3. Basal laminae create highly interactive surfaces that can promote cell migration and cell elongation during embryogenesis and wound repair. Following an injury, they provide a surface upon which cells regenerate to restore normal tissue function.

4. Basal laminae present information encoded in their structure to contacting cells that is important for differentiation and tissue maintenance. This information is communicated to the cells through various receptors that include the integrins, dystroglycan, and cell surface proteoglycans. Signaling is dependent not only on the presence of matrix ligands and corresponding receptors that interact with sufficient affinities, but also on such topographical factors as ligand density in a three-dimensional matrix "landscape", and on the ability of basal lamina components to cluster receptors. Because these matrix proteins can be long-lived, basal laminae create a "surface memory" in the basal lamina for resident and transient cells.

The basal lamina is largely composed of laminin and type IV collagen heterotrimers that in turn become organized into complex polymeric structures. To date, six type IV collagen chains and at least twelve laminin subunits have been identified. These chains possess shared and unique functions and are expressed with specific temporal (developmental) and spatial (tissue-site specific) patterns.

Laminins are a family of heterotrimeric glycoproteins that reside primarily in the basal lamina. They function via binding interactions with neighboring cell receptors, and by forming laminin networks, and they are important signaling molecules that can strongly influence cellular function. Laminins are important in both maintaining cell/tissue phenotype as well as promoting cell growth and differentiation in tissue repair and development.

Laminins are large, multi-domain proteins, with a common structural organization. The laminin molecule integrates various matrix and cell interactive functions into one molecule.

Laminin molecules are comprised of an α-, β-, and γ-chain subunit joined together through a coiled-coil domain. Within this structure are identifiable domains that possess binding activity towards other laminin and basal lamina molecules, and membrane-bound receptors. Domains VI, IVb, and IVa form globular structures, and domains V, IIIb, and IIIa (which contain cysteine-rich EGF-like elements) form rod-like structures. (Kamiguchi et al., Ann. Rev. Neurosci. 21:97-125 (1998)) Domains I and II of the three chains participate in the formation of a triple-stranded coiled-coil structure (the long arm).

Table 1 shows the individual chains that each laminin type is composed of:

TABLE 1. Known laminin family members

Protein	*Chains*
Laminin-1	α1β1γ1
Laminin-2	α2β1γ1
Laminin 3	α1β2γ1
Laminin-4	α2β2γ1
Laminin-5	α3β3γ2
Laminin-6	α3β1γ1
Laminin-7	α3β2γ1
Laminin-8	α4β1γ1
Laminin-9	α4β2γ1
Laminin-10	α5β1γ1
Laminin –11	α5β2γ1
Laminin-12	α2β1γ3

Four structurally-defined family groups of laminins have been identified. The first group of five identified laminin molecules all share the β1 and γ1 chains, and vary by their α-chain composition (α1 to α5 chain). The second group of five identified laminin molecules all share the β2 and γ1 chain, and again vary by their α-chain composition. The third group of identified laminin molecules has one identified member, laminin 5, with a chain composition of α3β3γ2. The fourth group of identified laminin molecules has one identified member, laminin 12, with the newly identified γ3 chain (α2β1γ3)

Some progress has been made in elucidating the relationship between domain structure and function. (See, for example, Wewer and Engvall, Neuromusc. Disord. 6:409-418 (1996).) The overall sequence similarity among the homologous domains in different chains varies, but it is highest in domain VI (thought to play a key role in laminin polymerization), followed by domains V (possibly involved in protein-protein interactions) and III (entactin/nidogen binding; possible cell adhesion sites), and is lowest in domains I, II (both thought to be involved in intermolecular assembly, and containing possible cell adhesion sites), and G. Not all domains are present in all 3 types of chains. The globular G domain (thought to be involved in cell receptor binding) is present only in the α chains. Other domains may not be present in all chains within a certain chain type. For example, domain VI is absent from α3, α4, and γ2 chains. (Wewer and Engvall, 1996)

As a result of their large size (>600 kD) and unique structure, laminin molecules can be resolved in the electron microscope. (Wewer and Engvall, 1996) Typically, laminins appear as cross-shaped molecules in an electron micrograph. The three short arms of the cross represent the amino terminal portions of each of the three separate laminin chains (one short arm per chain). The long arm of the cross is composed of the C-terminal parts of the three chains, which together form a coiled coil structure. (Wewer and Engvall, 1996) The long arm ends with the globular G domain.

The coiled-coil domain of the long arm is crucial for assembly of the three chains of laminin. (Yurchenco et al., Proc. Natl. Acad. Sci. 94:10189-10194 (1997)). Disulfide bonds bridge and stabilize all three chains in the most proximal region of the long arm and join the β and γ chains in the most distal region of the long arm.

A model of laminin receptor-facilitated self-assembly, based on studies conducted with cultured skeletal myotubes and Schwann cells, predicts that laminins bind to their receptors, which freely diffuse in a fluidic membrane when ligand-free. Receptor engagement forces the laminins into a high local two-dimensional concentration, facilitating their mass-action driven assembly into ordered surface polymers. In this process, the engaged receptors are also reorganized, accompanied by cytoskeletal rearrangements. (Colognato, J. Cell Biol. 145:619-631 (1999)) This reorganization activates the receptors, causing signal transduction with the alteration of cell expression, shape and/or behavior.

One class of laminin receptors are the integrins, which are cell surface receptors that mediate many cell-matrix and cell-cell interactions. Integrins are heterodimers, consisting of an α and a β subunit. 16 α- and 8 β-subunits are known, and at least 22 combinations of α and β subunits have been identified to date. Some integrins have only one or a few known ligands, whereas others appear to be very promiscuous. Binding to integrins is generally of low affinity, and is dependent on divalent cations. Integrins, activated through binding to their ligands, transduce signals via kinase activation cascades, such as focal adhesion and mitogen-activated kinases. Several different integrins bind different laminin isoforms more or less specifically. (Aumailley et al., In The Laminins, Timpl and Ekblom, eds., Harwood Academic Publishers, Amsterdam. pp. 127-158 (1996))

Laminin 2 is composed of α2 (400 kD), β1 (approximately 100 kD), and γ1 (approximately 100 kD) chains. The C-terminal G domain of the α2 chain forms a large globular structure responsible for binding to α-dystroglycan. (Kamiguchi et al., 1998).

The short arm domains of laminin 1 are involved in the self-aggregation process (Schittney and Yurchenco, J. Cell Biol. 110:825-832 (1990)) and with extracellular matrix components, such as type IV collagen. Homology between the α1 (laminin 1) and α2 chains is 58.6%. The significant homology between the α1 and α2 chains, especially in the N-terminal domains, and their identical β and γ chains, suggest that laminin 2 has a similar structural organization to laminin 1. (Kamiguchi et al., 1998)

Laminin 2 was originally found in the basement membranes of the placenta, striated muscle, and Schwann cells. (Leivo and Engvall, Proc. Natl. Acad. Sci. USA 85:1544-1548 (1998)) In normal adults, laminin 2 is predominant in the basal lamina of skeletal muscle, where it serves to provide mechanical reinforcement to the sarcolemma by linking the extracellular matrix and the subsarcolemmal cytoskeleton. (Sanes et al., J. Cell Biol. 111:1685-1699 (1990))

Genetic defects affecting the structure or expression of laminin 2 are the causes of a major type of congenital muscular dystrophy (CMD). Laminin 2 has been shown to be specifically required for stabilizing myotubes during skeletal muscle development, and for preventing apoptosis, which is believed to explain some of the pathological events observed in CMD. (Kamiguchi et al., 1998)

In vitro studies have demonstrated that partially purified laminin 2 is important for myotube survival and maintenance of phenotype. (Vachon et al., J. Cell Biol. 134:1483-1497 (1996)) In vivo experiments have shown partial laminin α2 chain restoration in a laminin α2 deficient, CMD animal model by primary muscle cell transplantation. (Vilquin et al., J. Cell Biol. 133:185-197)

Laminin 2 is also the predominant laminin isoform present in the endoneurial basement membrane of developing and mature peripheral nerves, and was shown to promote Schwann cell migration, neurite outgrowth, and neurite regeneration (Kamiguchi et al., 1998), as well as myelin formation by oligodendrocytes (Buttery et al., Mol. Cell. Neurosci. 14:199-212 (1999). The results of various experiments have indicated that laminin 2, rather than laminin 1, is important in Schwann cell/basal lamina interactions, especially at early developmental stages. (Kamiguchi et al., 1998) Other

studies have demonstrated that partially purified laminin 2 promotes neuronal cell migration and axon outgrowth (Agius and Cochard, J. Neurosci. 18:328-338 (1998); Kamiguchi et al, 1998; U.S. Patent Nos. 5,444,158; 5,872,231; 5,624,905; and 5,863,743; Bates and Meyer, Develop. Biol. 181:91-101 (1997)). In a laminin 2 deficient CMD animal model, CMD was accompanied by dysmyelination of peripheral motor nerves, indicating that laminin 2 plays an important role in peripheral myelinogenesis.

Partially purified laminin 2 has also been shown to promote cell migration and attachment to a substrate of a variety of cell types, particularly muscle cells and cells of neuronal origin. (U.S. Patent No. 5,444,158; White et al., Am. J. Resp. Biol. 20:787-796 (1999); Engvall et al., Exp. Cell Res. 198:115-123 (1992))

It has also been demonstrated that the molecular basis of the neural tropism of *Mycobacterium leprae* is attributable to the specific binding of *M. leprae* to the G domain of the laminin α2 chain on Schwann cell-axon units, while α-dystroglycan (αDG) was shown to serve as a Schwann cell receptor for *M. leprae*. (Rambukkana et al., Science 282:2076-2079 (1998); Rambukkana et al., Cell 88:811-821 (1997)). Native αDG was shown to competitively inhibit the laminin-2 mediated M. leprae binding to primary Schwann cells. (Rambukkana et al. 1998)

Thus, research and therapeutic applications for laminin 2 and fragments thereof include, but are not limited to, peripheral nervous system (PNS) nerve regeneration, treatment of degenerative muscle disorders, regulating angiogenesis, promoting cell attachment and migration, ex vivo cell therapy, improving the biocompatibility of medical devices, improving the "take" of grafts, and preparing improved cell culture devices and media.

At present, there is not a means to isolate adequate substantially purified laminin 2 from cell or tissue sources for research or therapeutic purposes, nor has a means been developed for production of recombinant heterotrimeric laminin 2. Laminin 2 can be partially purified from either placenta, or, in lesser amounts, from skeletal muscle. Human placenta has provided the only source for obtaining up to several milligrams of protein. (Cheng et al., J. Biol. Chem. 272:31525-32, 1997) However preparations of this laminin normally contain about an equal molar quantity of laminin 4 ($\alpha 2\beta 2\gamma 1$) and the protein nidogen (entactin). The nidogen is bound to the laminin through a fairly strong but non-covalent association. It is difficult to remove most of the laminin 4, and even after

additional steps, a significant contaminating level of laminin 4 remains. Denaturing conditions are required to remove the nidogen.

Therefore, there is a need in the art for adequate amounts of substantially purified laminin-2, and methods for making laminin 2. A preferred method of production is the use of recombinant DNA technology to engineer a cell line of choice to produce recombinant laminin-2. A recombinant-based method of laminin-2 production has several advantages over purification from tissue or isolation from cell lines in culture:

1. The recombinantly produced protein is free of pathogens. While this is also true for endogenous cell culture produced protein, protein derived from human tissue carries a risk for contamination by HIV, hepatitis, and other infectious agents.

2. Expression levels of the protein, and hence yields, can be improved through the use of genetically engineered genes/vectors that enhance the production of the encoded protein.

3. It is possible to engineer additional peptide sequences to the protein chain that provides a binding site for a commercially viable affinity purification procedure.

4. The method can provide for the modification of protein structure/function through the addition, substitution, elimination, and/or other modifications of protein domain structures. For example, it may be desirable to introduce an integrin binding site (e.g. RGD), switch integrin recognition sites, or engineer in a stable binding site to a synthetic substrate. Thus, the creation of expression vectors that express laminin chains generates enormous flexibility for future uses and creates a basis for creating second generation "designer" laminins.

Summary of the Invention

The present invention fulfills the need in the art for substantially purified laminin 2 protein, methods for making substantially purified recombinant laminin 2 (hereinafter referred to as r-laminin 2), and methods of using substantially purified laminin 2 for research and therapeutic purposes including, but not limited to, peripheral nerve regeneration, treatment of degenerative muscle disorders, angiogenesis regulation, promoting cell attachment and migration, ex vivo cell therapy, improving the "take" of

grafts, improving the biocompatibility of medical devices, and preparing improved cell culture devices and media

In one aspect, the present invention provides mammalian cells that have been transfected with expression vector(s) encoding at least one of the laminin α2, β1 and γ1 chains, wherein the cells secrete r-laminin 2.

In another aspect, the present invention provides substantially purified laminin 2 and methods for producing r-laminin 2.

In a further embodiment, the present invention provides a novel, isolated laminin 2 α2 nucleic acid and α2 protein. In this embodiment, the protein product contains an additional 30 amino acids at its carboxyl terminus relative to the previously reported sequence.

In a further aspect, the present invention provides pharmaceutical compositions, comprising substantially purified laminin 2, or the novel recombinant α2 protein together with a pharmaceutically acceptable carrier. Such pharmaceutical compositions can optionally be provided with other compounds, such as extracellular matrix components.

The present invention further provides methods for peripheral nerve regeneration, treatment of degenerative muscle disorders, regulating angiogenesis, promoting cell attachment and migration, ex vivo cell therapy, improving the biocompatibility of medical devices, improving the "take" of grafts, and preparing improved cell culture devices and media, comprising providing an amount effective of the substantially purified laminin 2, or pharmaceutical compositions thereof, for the desired outcome.

In a further aspect, the present invention provides improved medical devices or grafts, wherein the improvement comprises applying to the devices or grafts an amount effective of substantially purified laminin 2 or pharmaceutical compositions thereof, for the desired application. Such devices can optionally be provided with other compounds, such as extracellular matrix components to further improve the biocompatibility or the effectiveness of the medical device or graft.

In a further aspect, the invention provides improved cell culture devices, by providing an amount effective of substantially purified laminin 2, or pharmaceutical compositions thereof, for the attachment of cells to a cell culture device for the subsequent proliferation/differentiation/stasis of the cells.

In another aspect, the invention provides a cell culture growth supplement, comprising substantially purified laminin 2. In another aspect, the invention provides an

improved cell culture growth media, wherein the improvement comprises the addition of substantially purified laminin 2 to the growth medium.

Brief Description of the Figures

Figure 1 is a photograph of an Coomassie blue-stained SDS-polyacrylamide gel of recombinant laminin 2 compared to laminin 1.

Figure 2 is an electron micrographs of purified recombinant laminin 2.

Figure 3 is an immunoblot demonstrating the co-polymerization of laminin 2.

Figure 4 is a graph demonstrating C2C12 myoblast adherence to recombinant laminin 2.

Figure 5 shows the correct sequence of the laminin α2 cDNA and deduced amino acid sequence.

Detailed Description of the Preferred Embodiments

All references, patents and patent applications are hereby incorporated by reference in their entirety.

Within this application, unless otherwise stated, the techniques utilized may be found in any of several well-known references such as: *Molecular Cloning: A Laboratory Manual* (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), *Gene Expression Technology* (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, CA), "Guide to Protein Purification" in *Methods in Enzymology* (M.P. Deutshcer, ed., (1990) Academic Press, Inc.); *PCR Protocols: A Guide to Methods and Applications* (Innis, et al. 1990. Academic Press, San Diego, CA), *Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed.* (R.I. Freshney. 1987. Liss, Inc. New York, NY), *Gene Transfer and Expression Protocols*, pp. 109-128, ed. E.J. Murray, The Humana Press Inc., Clifton, N.J.), and the Ambion 1998 Catalog (Ambion, Austin, TX).

As used herein, "laminin 2" includes both r-laminin 2 and laminin 2 substantially purified from tissue sources.

As used herein, the term "r-laminin 2" refers to recombinant laminin 2, expressed by a cell that has been transfected with one or more expression vectors comprising at least one nucleic acid sequence encoding a laminin 2 chain selected from the α2, β1 and γ1 chains, processed forms thereof, or other portions thereof that are capable of forming a

heterotrimeric laminin 2 and maintaining laminin 2 activity. Such r-laminin 2 can thus comprise α2, β1, and γ1 sequences from a single organism, or from different organisms. Laminin 2 chain DNA sequences and their encoded proteins from a variety of organisms are known in the art. (See, for example, Vuolteenaho et al., J. Biol. Chem. 265:15611-15616 (1990); Kallunki et al., J. Biol. Chem. 266:221-228 (1991); Pikkarainen et al., J. Biol. Chem. 263:6751-6758 (1988); Sasaki and Yamada, J. Biol. Chem. 262:17111-17117 (1987); Sasaki et al., Proc. Natl. Acad. Sci. 84:935-939 (1987); Pikkarainen et al., J. Biol. Chem. 262:10454-10462 (1987); and Bernier et al., Matrix Biol. 14:447-455 (1995), all references incorporated by reference herein in their entirety).

The invention encompasses those laminin molecules wherein one or two of the chains that make up the recombinant heterotrimeric laminin 2 are encoded by endogenous laminin 2 chains. In a preferred embodiment, r-laminin 2 is produced by cells that are transfected with one or more expression vectors comprising nucleic acid sequences encoding each of mammalian α2, β1 and γ1 chains, processed forms thereof, or other portions thereof that are capable of forming a heterotrimeric laminin 2 and maintaining laminin 2 activity.

In the present invention, laminin 2 is a secreted protein, which is capable of being directed to the ER, secretory vesicles, and the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Such processing event can be variable, and thus may yield different versions of the final "mature protein". The substantially purified laminin 2 of the present invention includes heterotrimers comprising both the full length and any such processed laminin 2 chains.

As used herein, the term "substantially purified" means that the laminin 2 so designated has been separated from its in vivo cellular environment.

As used herein, a laminin 2 polypeptide chain refers to a polypeptide chain according to one or more of the following:

(a) comprises a polypeptide structure selected from the group consisting of:

1. R1-R2-R3
2. R1-R2-R3(e)
3. R3

4. R3(e)
5. R1-R3
6. R1-R3(e)
7. R2-R3
8. R2-R3(e)

wherein R1 is a amino terminal methioninc; R2 is a signal sequence that is capable of directing secretion of the polypeptide, wherein the signal sequence may be the natural signal sequence for the particular laminin chain, that of another secreted protein, or an artificial sequence; R3 is a secreted laminin chain selected from α2, β1, and γ1 chains; and R3(e) is a secreted laminin chain selected from the α2, β1, and γ1 chains that further comprises an epitope tag (such as those described below), which can be placed at any position within the laminin chain amino acid sequence; and/or

(b) is encoded by a polynucleotide that is substantially similar to on or more of the disclosed laminin chain polynucleotide sequences (SEQ ID NOS.: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31) or fragments thereof; and/or

(c) is encoded by a polynucleotide that hybridizes under high or low stringency conditions to coding regions, or portions thereof, of one or more of the recombinant laminin 2 chain DNA sequences disclosed herein (SEQ ID NOS.: 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31) fragments thereof, or complementary sequences thereof; and/or

(d) has at least 70% identity to one or more of the disclosed laminin 2 polypeptide chain amino acid sequences (SEQ ID NOS.: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or fragments thereof), preferably at least 80% identity, and most preferably at least about 90% identity.

The phrase "substantially similar" is used herein in reference to polynucleotide or polypeptide sequences having one or more conservative variations from the laminin 2 sequences disclosed herein, including but not limited to deletions, insertions, inversions, repeats, and substitutions, wherein the resulting laminin chain is functionally equivalent to those disclosed herein.

For example, conservative polynucleotide variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the amino acid sequence of the encoded polypeptide. Nucleotide variants

produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, including but not limited to optimizing codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring conservative variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level. Alternatively, non-naturally occurring conservative variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, conservative polynucleotide variants may be generated to improve or alter the characteristics of the expressed laminin chain polypeptides. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the secreted protein. (See, for example, Ron et al., J. Biol. Chem. 268: 2984-2988 (1993); Dobeli et al., J. Biotechnology 7:199-216 (1988)) Ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. (See, for example, Gayleet al., J. Biol. Chem 268:22105-22111 (1993)) Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained.

Guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, "substantially similar" polypeptides of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be "substantially similar" according to the present invention.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

"Stringency of hybridization" is used herein to refer to conditions under which nucleic acid hybrids are stable. The invention also includes nucleic acids that hybridize under high stringency conditions (as defined herein) to all or a portion of the coding sequences of the laminin chain polynucleotides disclosed herein, or their complements. The hybridizing portion of the hybridizing nucleic acids is typically at least 50 nucleotides in length. As known to those of skill in the art, the stability of hybrids is reflected in the melting temperature (T_M) of the hybrids. T_M decreases approximately 1-1.5°C with every 1% decrease in sequence homology. In general, the stability of a hybrid is a function of sodium ion concentration and temperature. Typically, the hybridization reaction is performed under conditions of lower stringency, followed by washes of varying, but higher, stringency. Reference to hybridization stringency relates to such washing conditions. Thus, as used herein, high stringency refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

Also contemplated are laminin 2-encoding nucleic acid sequences that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH_2PO_4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

As used herein, "percent identity" of two amino acids or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches are performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to the nucleic acid molecules of the invention. BLAST protein searches are performed with the XBLAST program, score = 50, wordlength = 3, to obtain an amino acid sequence homologus to a polypeptide of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids. Res. 25:3389-3402, 1997). When utilizing BLAST and Gapped BLAST programs, the default paramaters of the respective programs (e.g., XBLAST and NBLAST) are used. See http://www.ncbi.nlm.nih.gov.

Further embodiments of the present invention include polynucleotides encoding laminin 2 chain polypeptides having at least 70% identity, preferably at least 80% identity, and most preferably at least 90% identity to one or more polypeptide sequence contained in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, or fragments thereof.

As used herein, "α2 polynucleotide" refers to a polynucleotide encoding an α2 laminin chain of the same name. Such polynucleotides can be characterized by one or more of the following: (a) the nucleotides of said polynucleotide may encode an amino acid sequence substantially similar to one or more of the amino acid sequences set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12 or fragments thereof; (b) polynucleotides that encode polypeptides which share at least 70% identity, preferably 80% identity, and most preferably at least 90% identity with one or more of the sequences set forth in SEQ ID NO: 2, 4, 6, 8, 10, 12, or fragments thereof; (c) the α2 polynucleotides hybridize under low or high stringency conditions to the coding sequence set forth in one or more of SEQ ID NO: 1, 3, 5, 7, 9, 11, fragments thereof, or complementary sequences thereof; or (d) the α2 polynucleotides may encode a polypeptide with a general structure selected from (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e); wherein R1 and R2 are as described above, and R3 and R3(e) are as described above but comprise secreted α2 chain polypeptides.

As used herein, "β1 polynucleotide" refers to polynucleotides encoding a β1 laminin chain of the same name. Such polynucleotides can be characterized by one or more of the following: (a) the nucleotides of said polynucleotide may encode a polypeptide substantially similar to one or more of the amino acid sequences set forth in SEQ ID NO: 14, 16, 18, 20, or fragments thereof; (b) polynucleotides that encode polypeptides which share at least 70% identity, preferably at least 80%, and most preferably at least 90% identity with one or more of the sequences set forth in SEQ ID NO: 14, 16, 18, 20, or fragments thereof; (c) the β1 cDNAs hybridize under low or high stringency conditions to the coding sequence set forth in one or more of SEQ ID NO: 13, 15, 17, 19, fragments thereof, or complementary sequences thereof; or (d) the β1 polynucleotides may encode a polypeptide with a general structure selected from (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e); wherein R1 and R2 are as described above, and R3 and R3(e) are as described above but comprise secreted β1 chain polypeptides.

As used herein, "γ1 polynucleotide" refers to polynucleotides encoding a γ1 laminin chain of the same name. Such polynucleotides can be characterized by one or more of the following: (a) the nucleotides of said polynucleotide may encode an amino acid that is substantially similar to one or more of the sequences set forth in SEQ ID NO: 22, 24, 26, 28, 30, 32, or fragments thereof; (b) polynucleotides that encode polypeptides which share at least 70% identity, preferably at least 80%, and most preferably at least 90% identity with one or more of the sequences set forth in SEQ ID NO: 22, 24, 26, 28, 30, 32, or fragments thereof; (c) the γ1 polynucleotides hybridize under low or high stringency conditions to the coding sequence set forth in one or more of SEQ ID NO: 21, 23, 25, 27, 29, 31, fragments thereof, or complementary sequences thereof; or (d) the γ1 polynucleotides may encode a polypeptide with a general structure selected from (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e); wherein R1 and R2 are as described above, and R3 and R3(e) are as described above but comprise secreted γ1 chain polypeptides.

As used herein, the term "epitope tag" refers to a polypeptide sequence that is expressed as part of a chimeric protein, where the epitope tag serves as a recognition site for binding of antibodies generated against the epitope tag, or for binding of other molecules that can be used for affinity purification of sequences containing the tag.

As used herein, the term "increased biocompatibility" refers to reduced induction of acute or chronic inflammatory response, and reduced disruption of the proper differentiation of implant-surrounding tissues for laminin 2-coated biomaterials relative to an analogous, non-coated biomaterial.

In one aspect, the present invention provides r-laminin 2 expressing-cells that have been transfected with an expression vector containing promoter sequences that are operatively linked to nucleic acid sequences encoding at least one polypeptide sequence comprising the α2, β1 and γ1 chains of laminin 2, or fragments thereof, wherein the transfected cells secrete heterotrimeric laminin 2 containing the recombinant laminin chain. In a preferred embodiment, the cells are transfected with recombinant expression vectors containing promoter sequences that are operatively linked to nucleic acid sequences encoding polypeptide sequences comprising each of the mammalian α2, β1 and γ1 chains of laminin 2, or fragments thereof. After the transfection(s), the cells express each of the recombinant laminin 2 chains, which form the heterotrimer, before r-laminin 2 secretion into the media.

In a preferred embodiment, cDNAs encoding α2, β1 and γ1 laminin chains, or fragments thereof, are subcloned into an expression vector. Alternatively, laminin 2 α2, β1 and/or γ1 genomic sequences, including one or more introns, can be used.

Any cell capable of expressing and secreting the r-laminin 2 can be used. Preferably, eukaryotic cells are used, and most preferably mammalian cells are used, including but not limited to kidney and epithelial cell lines. In a most preferred embodiment, the mammalian cells do not express all of the laminin 2 chains endogenously. Carbohydrate and disulfide post-translational modifications are believed to be required for laminin 2 protein folding and function. This makes the use of eukaryotic cells preferable for producing functional r-laminin 2, although other systems are useful for obtaining, for example, antigens for antibody production.

"Recombinant expression vector" includes vectors that operatively link a nucleic acid coding region or gene to any promoter capable of effecting expression of the gene product. The promoter sequence used to drive expression of the individual chains or r-laminin 2 may be constitutive (driven by any of a variety of promoters, including but not limited to, CMV, SV40, RSV, actin, EF) or inducible (driven by any of a number of inducible promoters including, but not limited to, tetracycline, ecdysone, steroid-

responsive). The expression vector must be replicable in the host organisms either as an episome or by integration into host chromosomal DNA. In a preferred embodiment, the expression vector comprises a plasmid. However, the invention is intended to include other expression vectors that serve equivalent functions, such as viruses.

In one embodiment, at least one of the laminin chain polynucleotide sequences, or fragments thereof, is operatively linked to a nucleic acid sequence encoding an "epitope tag", so that at least one of the chains is expressed as a fusion protein with an expressed epitope tag. The epitope tag may be expressed as the amino terminus, the carboxy terminus, or internal to any of the polypeptide chains comprising r-laminin 2, so long as the resulting r-laminin 2 remains functional. Any epitope tag may be utilized, so long as it can be used as the basis for affinity purification of the resulting r-laminin 2. Examples of such epitope tags include, but are not limited to FLAG (Sigma Chemical, St. Louis, MO), myc (9E10) (Invitrogen, Carlsbad, CA), 6-His (Invitrogen; Novagen, Madison, WI), and HA (Boehringer Manheim Biochemicals).

In another embodiment, one of the r-laminin 2 chains is expressed as a fusion protein with a first epitope tag, and at least one other r-laminin chain is expressed as a fusion protein with a second epitope tag. This simplifies the purification procedure and facilitates higher recoveries. Alternatively, the same epitope tag can be used to create fusion proteins with more than one of the r-laminin chains.

In a further embodiment, the epitope tag can be engineered to be cleaveable from the r-laminin 2 chain(s). Alternatively, no epitope tag is fused to any of the r-laminin 2 chains, and the r-laminin 2 is purified by standard techniques, including but not limited to affinity chromatography using antibodies against laminin 2 antibodies or other laminin 2 binding molecules.

Transfection of the expression vectors into eukaryotic cells can be accomplished via any technique known in the art, including but not limited to calcium phosphate co-precipitation, electroporation, or liposome mediated-, DEAE dextran mediated-, polycationic mediated-, or viral mediated transfection. Transfection of bacterial cells can be done by standard methods.

In a preferred embodiment, the cells are stably transfected. Methods for stable transfection and selection of appropriate transfected cells are known in the art. In a most preferred embodiment, a CMV promoter driven expression vector is used in a human kidney embryonic 293 cell line.

In one example, media from cells transfected with a single laminin chain are initially analyzed on Western blots using laminin chain-specific antibodies. The expression of single laminin chains following transfection is generally intracellular. Clones showing reactivity against individual transfected chain(s) are verified by any appropriate method, such as PCR, reverse transcription-PCR, or nucleic acid hybridization, to confirm incorporation of the transfected gene. Preferably, analysis of genomic DNA preparations from such clones is done by PCR using laminin chain-specific primer pairs. Media from transfected clones producing all three chains are further analyzed for r-laminin 2 secretion and/or activity, by any appropriate method, including Western blot analysis and cell binding assays. Activity of the r-laminin 2 is preferably analyzed in cell adhesion and protein binding assays.

In another aspect, the present invention provides substantially purified laminin 2, preferably r-laminin 2. In one embodiment, the substantially purified laminin 2 comprises a first chain comprising an α2 chain polypeptide; a second chain comprising a β1 chain polypeptide; and a third chain comprising a γ1 chain polypeptide. Alternatively, the r-laminin 2 comprises a first chain that is substantially similar to at least one of the sequences shown in SEQ ID NO: 2, 4, 6, 8, 10, 12 or fragments thereof; a second chain that is substantially similar to at least one of the sequence shown in SEQ ID NO: 12, 14, 16, or 18, or fragments thereof; and a third chain that is substantially similar to the sequence shown in SEQ ID NO: 20, 22, 24, or 26, or fragments thereof.

In another embodiment, the substantially purified r-laminin 2 comprises a first chain comprising a polypeptide that is at least about 70% identical to at least one of the sequences shown in SEQ ID NO: 2, 4, 6, 8, or 10, or fragments thereof; a second chain comprising a polypeptide that is at least 70% identical to at least one of the sequences shown in SEQ ID NO: 14, 16, 18, 20, or fragments thereof; and a third chain comprising a polypeptide that is at least 70% identical to at least one of the sequences shown in SEQ ID NO: 22, 24, 26, 28, 30, 32, or fragments thereof, wherein the first, second, and third polypeptides assemble into a recombinant heterotrimeric laminin 2.

It is preferred that at least one of the first, second, or third chains of the substantially purified human r-laminin 2 is expressed as a fusion protein with an epitope tag.

Alternatively, the r-laminin 2 comprises a heterotrimeric polypeptide structure, wherein each individual chain comprises a general structure selected from the group

consisting of: (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e)

wherein R1 is a amino terminal methionine; R2 is a signal sequence that is capable of directing secretion of the polypeptide, wherein the signal sequence may be the natural signal sequence for the particular laminin chain, that of another secreted protein, or it may be an artificial sequence; R3 is a secreted α2, β1, or γ1 laminin chain; and R3(e) is a secreted laminin α2, β1, and γ1 chain that further comprises an epitope tag (such as those described above), which can be placed at any position within the laminin chain amino acid sequence.

In a preferred embodiment, purification of the r-laminin 2 is accomplished by passing media from the transfected cells through an affinity column. For example, antibodies or other binding molecules that bind to a peptide epitope expressed on at least one of the recombinant chains are attached to an affinity column, and bind r-laminin 2 that has been secreted into the media. The r-laminin 2 is removed from the column by passing excess peptide through the column. The eluted protein can subsequently be further purified, if desired.

Eluted fractions are analyzed by any appropriate method, including gel electrophoresis and Western blot analysis. In a further embodiment, the peptide epitope can be cleaved after purification. In other embodiments, two or three separate r-laminin chains are expressed as fusion proteins, each with a different epitope tag, permitting two or three rounds of purification and a doubly or triply purified r-laminin 2. The epitope tag can be engineered so as to be cleavable from the r-laminin 2 chain(s) after purification. Alternatively, no epitope tag is fused to any of the r-laminin 2 chains, and the r-laminin 2 is purified by standard techniques, including but not limited to affinity chromatography using laminin 2 specific antibodies or other laminin 2 binding molecules.

In another aspect, the present invention provides a novel polynucleotide encoding the laminin α2 chain, consisting of the sequence shown in SEQ ID NO:1. In another aspect, the present invention provides a novel laminin 2 α polypeptide chain, consisting of the sequence shown in SEQ ID NO:2. These sequences differ from the previously reported sequences, in that the laminin α2-chain encoding nucleic acid consists of an extra nucleotide, resulting in the nucleic acid encoding an additional 30 amino acids at the C-terminus over what has previously been reported.

The present invention further provides pharmaceutical compositions comprising substantially purified laminin 2, and a pharmaceutically acceptable carrier. In a preferred embodiment, the pharmaceutical composition comprises substantially purified r-laminin 2. According to this aspect of the invention, other agents can be included in the pharmaceutical compositions, depending on the condition being treated. The pharmaceutical composition may further comprise one or more other compounds, including but not limited to any of the collagens, other laminin types, fibronectin, vitronectin, cadherins, integrins, α-dystroglycan, entactin/nidogen, α-dystroglycan, glycoproteins, proteoglycans, heparan sulfate proteoglycan, glycosaminoglycans, epidermal growth factor, vascular endothelial growth factor, fibroblast growth factor, or nerve growth factors, and peptide fragments thereof. In an alternative embodiment, the pharmaceutical compositions comprise the novel laminin α2 polypeptide chain of the invention together with a pharmaceutically acceptable carrier.

Pharmaceutical preparations comprising substantially purified laminin 2 can be prepared in any suitable form, and generally comprise the substantially purified laminin 2 in combination with any of the well known pharmaceutically acceptable carriers. The carriers can be injectable carriers, topical carriers, transdermal carriers, and the like. The preparation may advantageously be in a form for topical administration, such as an ointment, gel, cream, spray, dispersion, suspension or paste. The preparations may further advantageously include preservatives, antibacterials, antifungals, antioxidants, osmotic agents, and similar materials in composition and quantity as is conventional. Suitable solutions for use in accordance with the invention are sterile, are not harmful for the proposed application, and may be subjected to conventional pharmaceutical operations such as sterilization and/or may contain conventional adjuvants, such as preservatives, stabilizers, wetting agents, emulsifiers, buffers etc. For assistance in formulating the compositions of the present invention, one may refer to Remington's Pharmaceutical Sciences, 15th Ed., Mack Publishing Co., Easton, Pa. (1975).

In further aspect, the present invention provides methods and kits for peripheral nerve regeneration, treatment of degenerative muscle disorders, regulating angiogenesis, promoting cell attachment and migration, ex vivo cell therapy, improving the biocompatibility of medical devices, improving the "take" of grafts, and preparing improved cell culture devices and media, comprising providing an amount effective of the

substantially purified laminin 2, or pharmaceutical compositions thereof for the desired outcome. In all of these methods, the use of r-laminin 2 is preferred.

As used herein, the term "grafts" refers to both natural and prosthetic grafts as well as implants.

The treatment of peripheral nerve injuries is a common surgical problem. Nerve injuries can result from trauma, chronic compression, ischemia, radiation, errors of therapy and other causes. The severe forms of injury, in which the nerve is partially or completely disrupted, are difficult or impossible to treat by existing therapies. The basal lamina plays a key role in providing a migration guide for regenerating axons and Schwann cells following such nerve injury. The prognosis for successful regeneration is significantly better if the basement membrane remains intact.

Recently, the feasibility of using basal lamina coated bio-materials as a workable graft was demonstrated in a rat model in two studies (Kauppila *et al.*, Exp. Neurol. 123:181-191 (1993); Tong *et al.*, Brain Res. 663:155-162). In the first study, a bovine tendon collagen I graft sheet was impregnated with partially purified, non-recombinant mouse laminin-1, with the cut ends of the rat sciatic nerve (8 mm removed) sutured to the ends of the rolled graft. Function to the affected limb, as judged by electrophysiological and behavioral measurements at 4 months post-operatively, was restored (~60-80% relative to unaffected contralateral nerve) with the laminin graft at a level equivalent to restoring the transected nerve segment. The authors further reported that the laminin graft caused fewer signs of pain. In the second study, the authors created a graft by coating collagen fibrils with purified, non-recombinant laminin and fibronectin, and inserting the modified fibrils in a collagen sleeve. This graft, about 1 cm in length, was again sutured to the proximal and distal end of a transected sciatic nerve. Axonal/Schwann cell growth occurred into the graft with ultimate reattachment with the distal nerve stump. By light and electron microscopy, restoration of essential structural/cellular elements was found in the graft with ultimate resorption of the graft material. The laminin/fibronectin coat was essential since the collagen fibrils alone were not sufficient to restore the nerve.

The studies of Kauppila *et al.* and Tong *et al.* not only demonstrate the value of basal lamina components in regeneration, but also demonstrate therapeutic feasibility. A similar method for enhancing nerve regeneration using a hollow nerve regeneration conduit coated with type I collagen and purified placental laminin (predominately laminin 1) has also been disclosed. (U.S. Patent No. 5,019,087)

Thus, in one embodiment, the present invention provides methods to promote peripheral nerve regeneration, comprising coating a nerve graft with an amount effective of substantially purified laminin 2, or pharmaceutical compositions thereof, to promote regeneration of the nerve. Laminin 2 is the predominant laminin isoform present in the endoneurial basement membrane of developing and mature peripheral nerves, and was shown to promote neuronal cell migration and regeneration, axon outgrowth, myelin membrane formation by oligodendrocytes, and Schwann cell migration. (Kamiguchi et al., (1998); Agius and Cochard, J. Neurosci. 18:328-338 (1998); U.S. Patent No. 5,444,158; Buttery et al., Mol. Cell. Neurosci. 14:199-212 (1999); Bates and Meyer, Develop. Biol. 181:91-101 (1997)). The present invention provides a plentiful supply of substantially purified laminin 2, or pharmaceutical compositions thereof, for coating nerve grafts, and thereby promoting neuronal and Schwann cell migration, axonal migration, myelin membrane formation, and nerve regeneration. The graft can comprise a nerve graft, or a prosthetic graft. Both bioresorbable and non-resorbable materials have been used in tubes for bridging nerve gaps. (See for example, Nyilas, et al., (Trans. Soc. Biomater., 6, 85, 1983), Molander, et al. (Biomaterials, Vol. 4, pp. 276-280, October, 1983), Colin, et al., (Journal of Dental Research July, 1984, pp. 987-993).

In another embodiment, r-laminin 2 is used to promote the healing of degenerative muscle disorders. Laminin 2 is known to be important for myotube survival and maintenance of phenotype. (Vachon et al., J. Cell Biol. 134:1483-1497 (1996)). In vitro studies have demonstrated that partially purified laminin 2 promotes myoblast fusion and myotube formation. (Vachon et al., J. Cell Biol. 134:1483-1497 (1996)) In vivo experiments have shown partial laminin α2 chain restoration in a laminin α2 deficient, CMD animal model by primary muscle cell transplantation. (Vilquin et al., J. Cell Biol. 133:185-197 (1996)) Thus, mammalian cells that express r-laminin 2, or the novel laminin α2 chain of the invention, can be used for cell therapy, to treat patients with degenerative muscle disorders such as muscular dystrophies that are characterized by a laminin α2 deficiency.

Partially purified laminin 2 has also been shown to promote the migration of and attachment to a substrate of a variety of cell types, particularly muscle cells and cells of neuronal or mesenchymal origin. (U.S. Patent No. 5,444,158; White et al., Am. J. Resp. Biol. 20:787-796 (1999); Engvall et al., Exp. Cell Res. 198:115-123 (1992))

Thus, in another embodiment, substantially purified laminin 2, or pharmaceutical compositions thereof, can be added to medical devices, tissue culture plates, grafts, and cell culture media to provide important ligand substrates to maintain and expand primary explanted human tissue cells. This takes advantage of what has been observed by many investigators over the past decade, i.e., basal lamina components, in particular laminins, provide optimal surfaces for the adhesion, spreading, propagation, and maintenance of the differentiated phenotype of a large variety of cells. This property of substantially purified laminin 2 can be exploited to increase the biocompatibility of a medical device, to permit the maintenance of human cells in a laboratory affording time to find a suitable donor, and for the expansion of cell populations for transplantation and somatic gene therapy. Possible target cells for *ex vivo* therapy include cells of muscle and neuronal origin, lymphocytes and cells of the immune system, pancreatic islet, parathyroid, adrenal, pituitary, hepatic, cardiac muscle and stem cells.

In another embodiment, the present invention provides methods for regenerating cells and tissues both *in vivo* and *ex vivo*. Many of the current approaches for tissue engineering begin with a collagen/polymer scaffolding that is seeded with appropriate cells that can proliferate and differentiate into cell masses and tissue sub-structures. In the development of these methods, attempts have been made to add coatings to the scaffolding to provide for a more natural surface for cell interactions, with the expectation that cell proliferation and tissue development would be enhanced. Coating these matrices with the substantially purified laminin 2 provides for a natural ligand interactive surface to promote normal cell adherence, cell growth and tissue development. Thus, the availability of substantially purified laminin 2 is expected to significantly improve tissue regeneration procedures.

Laminins, or cell extracts containing laminins, have been shown to regulate angiogenesis in a biphasic manner. (See, for example, Nicosia et al., Dev. Biol. 164:197-206 (1994); Bonfil et al., Int. J. Cancer 58:233-239 (1994)). At lower concentrations (30-300 μg/ml), a laminin-entactin complex stimulated angiogenesis in a three-dimensional culture, while at 3000 μg/ml the same complex was inhibitory to angiogenesis. Thus, in another aspect, the present invention provides methods for regulating angiogenesis, comprising contacting a tissue or culture substrate with an amount effective of laminin 2 or pharmaceutical compositions thereof to regulate angiogenesis. In one embodiment, the laminin 2 is used to promote angiogenesis by contacting a tissue or culture substrate with

an amount effective of laminin 2 to promote angiogenesis. In another embodiment, the laminin 2 is used to inhibit angiogenesis, by contacting the tissue or culture substrate with an amount effective of laminin 2 to inhibit angiogenesis. An example of culture substrates to be contacted with laminin 2 to regulate angiogenesis are those used for tissue engineering purposes.

In a further aspect, the present invention comprises medical devices with improved biocompatibility, wherein the devices are coated with the substantially purified laminin 2, or pharmaceutical compositions thereof, alone or in combination with other proteins or agents that serve to increase the biocompatibility of the device surface. The coated device stimulates cell attachment and provides for diminished inflammation and/or infection at the site of entry of the appliance.

Preferably, the device is made of or coated with a biocompatible metal that may be either stainless steel or titanium. Alternatively, the device is made of or coated with a ceramic material, or a polymer including but not limited to polyester, polyglycolic acid or a polygalactose-polyglycolic acid copolymer.

One particular use of the present invention is to increase neuronal, skeletal muscle, endothelial or mesenchymal cell adhesion to target surfaces. For example, vascular grafts and stents may be coated with substantially purified laminin 2 to stimulate endothelial cell attachment, and to minimize platelet adhesion to the graft or stent surface. Alternatively, bone or connective tissue grafts or prostheses may be coated with substantially purified laminin 2 to stimulate adhesion of the appropriate cell type and improved efficiency of grafting.

If the device is made of a natural or synthetic biodegradable material in the form of a mesh, sheet or fabric, substantially purified laminin 2 may be applied directly to the surface thereof. Appropriate cells may then be cultured on the matrix to form transplantable or implantable devices, including dental abutment pieces, needles, metal pins or rods, indwelling catheters, colostomy tubes, surgical meshes and any other appliance for which coating with the substantially purified laminin 2 is desirable. Alternatively, the devices may be implanted and cells may be permitted to attach in vivo.

Coupling of the substantially purified laminin 2 may be non-covalent (such as by adsorption), or by covalent means. The device may be immersed in, incubated in, or sprayed with substantially purified laminin 2 or pharmaceutical compositions thereof.

The dosage regimen for various treatments using the substantially purified laminin

2 of the present invention is based on a variety of factors, including the type of injury or condition, the age, weight, sex, medical condition of the individual, the severity of the condition, and the route of administration. Thus, the dosage regimen may vary widely, but can be determined routinely by a physician using standard methods. Laminins are extremely potent molecules, and one or a few molecules per cell could produce an effect. Thus, effective doses in the pico-gram per milliliter range are possible if the delivery is optimized. Laminins are sometimes present in an insoluble form in the basement membrane and have the capability of polymerizing at concentrations as low as about 50 μg/ml, depending on the laminin isoform and the conditions. Laminins can also polymerize into a gel at a concentration of 2-3 mg/ml. Dosage levels of the order of between 1 ng/ml and 10 mg/ml are thus useful for all methods disclosed herein, preferably between about 1 μg/ml and about 3 mg/ml.

The present invention also provides a method for inducing cell attachment to the device (as disclosed above), comprising coating the appliance with substantially purified laminin 2 prior to incubation with cells appropriate for the desired application.

In another aspect of the present invention, substantially purified laminin 2 is used for the culture of cells, including but not limited to neuronal, skeletal muscle, fibroblasts, Schwann cells, cells of mesenchymal origin, and endothelial cells, by contacting the cells with an amount effective of substantially purified laminin 2 to stimulate attachment and proliferation/differentiation/stasis of cells. The substantially purified laminin 2 can either be provided in the cell culture medium, or as a cell culture medium supplement, or may be coated on the surface of a cell growth substrate. In a preferred embodiment, the method further includes contacting the cells with other compounds, including but not limited to any of the collagens, other laminin types, fibronectin, vitronectin, cadherins, entactin/nidogen, α-dystroglycan, glycoproteins, proteoglycans, heparan sulfate proteoglycan, glycosaminoglycans, epidermal growth factor or nerve growth factors, and peptide fragments thereof.

The cells may comprise primary cells or cell culture cell lines. The methods of this aspect of the invention can be used in vivo, ex vivo, or in vitro.

In a preferred embodiment, r-laminin 2 is used to coat the surface of a substrate, to promote cell adhesion to the substrate, and to stimulate cell proliferation/differentiation/stasis. The substrate used herein may be any desired substrate. For laboratory use, the substrate may be as simple as glass or plastic. For use in

vivo, the substrate may be any biologically compatible material capable of supporting cell growth. Suitable substrate materials include shaped articles made of or coated with such materials as collagen, regenerated collagen, polyglycolic acid, polygalactose, polylactic acid or derivatives thereof; biocompatible metals such as titanium and stainless steel; ceramic materials including prosthetic material such as hydroxylapatite; synthetic polymers including polyesters and nylons; polystyrene; polyacrylates; polytetrafluoroethylene and virtually any other material to which biological molecules can readily adhere.

In a further aspect, the present invention provides cell growth substrates for the adhesion and proliferation of cells in culture, by providing an amount effective of substantially purified laminin 2 for the attachment of cells to a cell culture device for the attachment and subsequent proliferation, differentiation, or stasis of the cells. The substrates may comprise any of the substrates discussed above. Preferably, r-laminin 2 is coated on the surface of the substrate at a concentration of between about 1 ng/ml and about 10 mg/ml, and more preferably 1 ng/ml and about 10 μg/ml.

In another aspect of the present invention, an improved cell culture medium is provided, wherein the improvement comprises addition to the cell culture medium of an effective amount of substantially purified laminin 2 to the cell culture medium to promote the adherence, proliferation, differentiation, or stasis of cells. Any cell culture media that can support the growth of cells can be used with the present invention. Such cell culture media include, but are not limited to Basal Media Eagle, Dulbecco's Modified Eagle Medium, Iscove's Modified Dulbecco's Medium, McCoy's Medium, Minimum Essential Medium, F-10 Nutrient Mixtures, Opti-MEM® Reduced-Serum Medium, RPMI Medium, and Macrophage-SFM Medium or combinations thereof.

The improved cell culture medium can be supplied in either a concentrated (ie: 10X) or non-concentrated form, and may be supplied as either a liquid, a powder, or a lyophilizate. The cell culture may be either chemically defined, or may contain a serum supplement. Culture media is commercially available from many sources, such as GIBCO BRL (Gaithersburg, MD) and Sigma (St. Louis, MO). In an alternative embodiment, the r-laminin 2 is used as a cell culture supplement.

The present invention may be better understood with reference to the accompanying examples that are intended for purposes of illustration only and should not be construed to limit the scope of the invention, as defined by the claims appended hereto.

Examples

Recombinant Laminin-2

cDNAs coding for the complete open reading frame of the human β1 chain and the human γ1 chain have been described. (Kallunki et al., J. Biol. Chem. 266:221-228 (1991); Pikkarainen et al., J. Biol. Chem. 262:10454-10462 (1987); Pikkarainen et al., J. Biol. Chem. 263:6751-6758 (1988); Pikkarainen et al., Eur. J. Biochem. 209:571-582 (1992)). The γ1 cDNA was modified to contain a 3' end (corresponding to the C-terminal end) insertion coding for the FLAG peptide epitope tag (SEQ ID NO:25). The complete human laminin α2 cDNA was constructed from the large (approximately 2/3 of open reading frame) cDNA as described in (Vuolteenaho et al., J. Cell Biol. 124:381-394 (1994)) with the C-terminal (3'-end) cDNA as described in (Ehrig et al., Proc. Natl. Acad. Sci. 87:3264-3268 (1990)). The β1, γ1, and α2 cDNAs were inserted into the pCIS (Genentech, South San Francisco, CA), pRC-CMV, and pCEP4 (InVitrogen, Inc., Carlsbad, CA) mammalian expression vectors respectively. pRC-CMV contained a neo (G418) expression cassette and pCEP4 contained a puromycin expression cassette, each under a separate promoter. Transfection of human embryonic kidney 293 cells (adenovirus transformed, ATCC CRL 1573) with the γ1-FLAG expression vector was carried out by calcium phosphate precipitation in 35 mm plastic dishes as previously described (Yurchenco et al., Proc. Natl. Acad. Sci. 94:10189-94 (1997)). Laminin γ1 expressing stable clones were selected in the presence of G418 antibiotic. These cells were found to express the laminin γ1 chain that reacted with both laminin and FLAG-specific antibodies in immunoblots. One such clone was subsequently co-transfected with the expression vector DNA coding for the α2 and β1 laminin chains. New clones were selected in the presence of G418+ puromycin. A clone (designated #44) was determined to express all three laminin 2 chains, by using polyclonal antibodies specific for placental laminin and the α2-G domain, β1 chain, and FLAG epitope tag (Cheng et al., J. Biol. Chem. 272:31525-32 (1997); Rambukkana et al., Cell 88:811-821 (1997)). This clone was expanded in tissue culture. Conditioned serum-containing medium was collected and pooled for purification of secreted protein.

Purification of recombinant laminin 2

The procedure is described for 100 ml of pooled conditioned medium. Purification was carried out at 4°-10°C in a cold room. A small column was packed with two ml of heparin-Sepharose-4B beads and equilibrated with Tris-buffer (50 mM Tris-HCl, pH 7.4, containing 1 MM EDTA and 0.1 mM PMSF) diluted 2:1 with water. The medium was passed through the column. The column was then washed with several volumes of Tris-buffer to decrease the NaCl concentration. One ml of anti-FLAG M2 agarose affinity gel suspension (Sigma-Aldrich, St. Louis, MO) was added to the preparation and used to absorb the recombinant protein bearing the FLAG epitope tag. After washing five times with Tris-buffer, 0.1 mg (in one ml) of FLAG peptides (Sigma-Aldrich) was added to elute the recombinant laminin protein from the beads. The protein was freed of peptides with a spin column. Recombinant protein was characterized by SDS-polyacrylamide gel electrophoresis (SDS-PAGE) (**Figure 1**), immunoblotting, and Pt/C rotary shadow electron microscopy (**Figure 2**).

Recovered yields of recombinant laminin 2 were 6 μg/ml purified protein from conditioned medium (determined from a 100 ml batch preparation). The recombinant laminin had three Coomassie blue-staining bands, the larger corresponding to the α2 subunit. (Figure 1) Some unprocessed (i.e.: uncleaved) α2 chain was typically observed. The cleaved version contained a high molecular weight band (approximately 300 kDa) and a 75 kDa band, the latter the predicted G fragment. (Cheng et al., J. Biol. Chem. 272:31525-32 (1997) The two forms of laminin 2 could be separated from each other by heparin affinity chromatography.

Figure 2 is an electron micrograph of purified r-laminin 2, which was dialyzed into 0.15M ammonium bicarbonate, mixed with glycerol to a final ratio of 6:4 glycerol:buffer, and nebulized onto freshly cleraved mica. The sample was evacuated in a Balzars BAF-500K freeze-etch unit and rotary shadowed at an 8° angle with 0.9 nm Pt/C as described (Yurchenco et al., Proc. Natl. Acad. Sci. 94:10189-94 (1997)). As can be seen from the figure, r-laminin 2 demonstrates the cruciform structure that is typical of endogenously expressed laminin molecules.

Functional Data

Recombinant laminin 2 was found to possess self-assembly activity in a co-polymerization assay (**Figure 3**). A fixed trace amount of r-laminin 2 was mixed with increasing concentrations of laminin 1 in separate tubes (each containing a small amount

of bovine serum albumin (BSA)) and incubated at 37μC as described (Cheng et al., J. Biol. Chem. 272:31525-32 (1997)). The incubation mixtures were then centrifuged in supernatant (S) and polymer pellet (P) fractions. Laminin 2 was detected with FLAG-specific antibody. At higher conentrations, increasing fractions of laminin 2 are detected in the pellet fraction, evidence for laminin-type polymerization.

R-laminin 2 was also found to support adhesion and spreading of C2C12 myoblasts (**Figure 4**), but not HT1080 fibrosarcoma cells (data not shown). Cultured myoblasts were added to 96-well culture dishes previously coated with two preparations of r-laminin 2 (two left bars), or with r-laminin 2 bearing different deletions of the G domain, all at 5 μg/ml. Deletion of G1-3 sub-domains (which bears the α7β1 integrin binding site), or all of G (which also removes the dystroglycan sites) greatly reduced binding.

Human laminin α2 polynucleotide and polypeptide

We have determined that the published sequence of the human laminin α2 nucleic acid and protein sequences (Ehrig et al., PNAS 87:3264-3268 (1990) are incorrect. An erroneous dropped G base that should lie near the 3' end of the nucleic acid sequence (**Figure 5**), leads to a prediction of a prematurely truncated laminin alpha2-G domain. The correct amino acid sequence for the α2 chain protein is shown in **Figure 5.**

One of the most serious consequences of the erroneous sequence may be that the end of the G domain is predicted to lack a cysteine residue that is conserved in different laminins, and is present in the corrected sequence presented here. It is thought that this cysteine pairs with another cysteine in the G domain and is important for protein conformation. Furthermore, if the incorrect sequence is used, an epitope tag placed at the apparent C-terminus will in fact be out of frame, and thus the epitope tag will not be functional.

The present invention is not limited by the aforementioned particular preferred embodiments. It will occur to those ordinarily skilled in the art that various modifications may be made to the disclosed preferred embodiments without diverting from the concept of the invention. All such modifications are intended to be within the scope of the present invention.

Claims

We claim

1. Substantially purified laminin 2.

2. The substantially purified laminin 2 of claim 1, comprising recombinant laminin 2.

3. The substantially purified recombinant laminin 2 of claim 2 comprising:

a first chain comprising a polypeptide that is substantially similar to an α2 laminin chain;

a second chain comprising a polypeptide that is substantially similar to a β1 laminin chain; and

a third chain comprising a polypeptide that is substantially similar to a γ1 laminin chain;

wherein the first, second, and third chains are assembled into recombinant heterotrimeric laminin 2.

4. The substantially purified recombinant laminin 2 of claim 2 comprising:

a first chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more of SEQ ID NO:1, 3, 5, 7, 9, 11, or fragments thereof;

a second chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more of SEQ ID NO:13, 15, 17, 19 or fragments thereof; and

a third chain encoded by a polynucleotide that hybridizes under high stringency conditions to a coding region of one or more of SEQ ID NO: 21, 23, 25, 27, 29, 31 or fragments thereof;

wherein the first, second, and third chains are assembled into recombinant heterotrimeric laminin 2.

5. The substantially purified recombinant laminin 2 of claim 2 comprising:

a first chain comprising a polypeptide at least 70% identical to one or more of SEQ ID NO:2, 4, 6, 8, 10, 12 or fragments thereof;

a second chain comprising a polypeptide at least 70% identical to one or more of

SEQ ID NO:14, 16, 18, 20 or fragments thereof; and

a third chain comprising a polypeptide at least 70% identical to one or more of SEQ ID NO:22, 24, 26, 28, 30, 32, or fragments thereof;

wherein the first, second, and third chains are assembled into recombinant heterotrimeric laminin 2.

6. The substantially purified recombinant laminin 2 of claim 2 comprising a first, second, and third polypeptide chain, wherein the first, second, and third polypeptide chains each comprise a general structure selected from the group consisting of: (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e)

wherein R1 is a amino terminal methionine; R2 is a signal sequence that is capable of directing secretion of the polypeptide, wherein the signal sequence may be the natural signal sequence for the particular laminin chain, that of another secreted protein, or it may be an artificial sequence; R3 is a secreted α2 laminin chain for the first polypeptide chain, a secreted β1 laminin chain for the second polypeptide chain, and γ1 laminin chain for the third polypeptide chain; and R3(e) is identical to R3, but further comprises an epitope tag.

7. Recombinant laminin 2-expressing host cells.

8. The recombinant laminin 2-expressing host cells of claim 7, wherein the cells express recombinant laminin 2 comprising:

a first chain comprising a recombinant polypeptide that is substantially similar an laminin α2 polypeptide;

a second chain comprising a recombinant polypeptide that is substantially similar to a laminin β1 polypeptide sequence; and

a third chain comprising a recombinant polypeptide that is substantially similar to a laminin γ1 polypeptide sequence;

wherein the cell expresses the first, second, and third chains, and wherein the first, second, and third chains assemble into recombinant laminin 2 that is secreted into the media by the cultured cell.

9. The recombinant laminin 2-expressing host cells of claim 7, wherein the cells express recombinant laminin 2 comprising:

a first chain encoded by a polypeptide that hybridizes under high stringency conditions to a coding region of one or more of SEQ ID NO:1, 3, 5, 7, 9, 11, or fragments thereof;

a second chain encoded by a polypeptide that hybridizes under high stringency conditions to a coding region of one or more of SEQ ID NO:1, 15, 17, 19, or fragments thereof; and

a third chain encoded by a polypeptide that hybridizes under high stringency conditions to a coding region of one or more of SEQ ID NO: 21, 23, 25, 27, 29, 31, or fragments thereof;

wherein the cell expresses the first, second, and third chains, and wherein the first, second, and third chains assemble into recombinant laminin 2 that is secreted into the media by the cultured cell.

10. The recombinant laminin 2-expressing host cells of claim 7, wherein the cells express recombinant laminin 2 comprising:

a first chain comprising a polypeptide at least 70% identical to one or more of SEQ ID NO:2, 4, 6, 8, 10, 12, or fragments thereof;

a second chain comprising a polypeptide at least 70% identical to one or more of SEQ ID NO:14, 16, 18, 20, or fragments thereof; and

a third chain comprising a recombinant polypeptide at least 70% identical to one or more of SEQ ID NO:22, 24, 26, 28, 30, 32, or fragments thereof;

wherein the cell expresses the first, second, and third chains, and wherein the first, second, and third chains assemble into recombinant laminin 2 that is secreted into the media by the cultured cell.

11. The recombinant laminin 2-expressing host cells of claim 7, wherein the cells express recombinant laminin 2 comprising a first, second, and third polypeptide chain, wherein the first, second, and third polypeptide chains each comprise a general structure selected from the group consisting of: (1) R1-R2-R3; (2) R1-R2-R3(e); (3) R3; (4) R3(e); (5) R1-R3; (6) R1-R3(e); (7) R2-R3; and (8) R2-R3(e)

wherein R1 is a amino terminal methionine; R2 is a signal sequence that is capable of directing secretion of the polypeptide, wherein the signal sequence may be the natural signal sequence for the particular laminin chain, that of another secreted protein, or it may be an artificial sequence; R3 is a secreted α2 laminin chain for the first polypeptide chain, a secreted β1 laminin chain for the second polypeptide chain, and γ1 laminin chain for the third polypeptide chain; and R3(e) is identical to R3, but further comprises an epitope tag .

12. The host cells of any of claims 7-11, wherein the host cell is a mammalian cell.

13. The host cells of claim 12, wherein at least one of the first, second, or third chains is expressed as a fusion protein with an epitope tag.

14. A method of purifying recombinant laminin 2, comprising:

a. providing the host cells of claim 12;

b. growing the cells in cell culture medium under conditions to stimulate expression of the recombinant laminin 2 chains;

c. passing the cell culture medium through an affinity chromatography column, wherein the column contains a compound that binds to the recombinant laminin 2;

d. washing the affinity column to remove unbound materials; and

e. eluting the bound recombinant laminin 2 from the column.

15. Substantially purified recombinant laminin 2 isolated according to the method of claim 14.

16. A pharmaceutical composition comprising:

a. laminin 2; and

b. a pharmaceutically acceptable carrier.

17. The pharmaceutical composition of claim 16, wherein the laminin 2 comprises recombinant laminin 2.

18. A method to promote nerve regeneration in a mammal, comprising administering to a mammal in need thereof an amount effective of the laminin 2 of any of claims 1-5 and 15 to promote nerve regeneration.

19. A method for regulating angiogenesis, comprising contacting a tissue in need thereof with an amount effective to regulate angiogenesis of the laminin 2 of any of claims 1-5 and 15 to regulate angiogenesis.

20. A method to improve the biocompatibility of a medical device, comprising contacting the medical device with an amount effective of the laminin 2 of any of claims 1-5 and 15 to improve the biocompatibility of the medical device.

21. An improved medical device, comprising a medical device with an amount effective of the laminin 2 of any of claims 1-5 and 15 to improve the biocompatibility of the medical device.

22. A method to promote cell adhesion to a surface, comprising contacting cells with an amount effective of the laminin 2 of any of claims 1-5 and 15 to promote cell adhesion to a surface.

23. An improved cell growth surface, wherein the improvement consists of providing a cell growth surface that has been coated with an amount effective of the laminin 2 of any of claims 1-5 and 15 to promote cell attachment to the cell growth surface.

24. A method to promote nerve regeneration in a mammal, comprising administering to a mammal in need thereof an amount effective of the pharmaceutical composition of claim16 or 17 to promote nerve regeneration.

25. A method for regulating angiogenesis, comprising contacting a tissue in need thereof with an amount effective to regulate angiogenesis of the pharmaceutical composition of claim 16 or 17 to regulate angiogenesis.

26. A method to improve the biocompatibility of a medical device, comprising contacting the medical device with an amount effective of the pharmaceutical composition of claim 16 or 17 to improve the biocompatibility of the medical device.

27. An improved medical device, comprising a medical device with an amount effective of the pharmaceutical composition of claim 16 or 17 to improve the biocompatibility of the medical device.

28. A method to promote cell adhesion to a surface, comprising contacting cells with an amount effective of the pharmaceutical composition of claim 16 or 17 to promote cell adhesion to a surface.

29. An improved cell growth surface, wherein the improvement consists of providing a cell growth surface that has been coated with an amount effective of the pharmaceutical composition of claim 16 or 17 to promote cell attachment to the cell growth surface.

30. An isolated recombinant laminin α2 chain polynucleotide consisting essentially of the sequence shown in SEQ ID NO:1.

31. A substantially purified laminin α2 chain polypeptide consisting essentially of the sequence shown in SEQ ID NO:2.

32. An expression vector comprising the polynucleotide of SEQ ID NO:1.

33. A host cell transfected with the expression vector of claim 32.

34. A method for treating degenerative muscle disorders in a mammal, comprising administering the host cells of any of claims 7-13 and 33 to a mammal in need thereof, wherein the host cells secrete an amount effective of the recombinant laminin 2 or the recombinant laminin α2 chain polypeptide, to treat the degenerative muscle disorder.

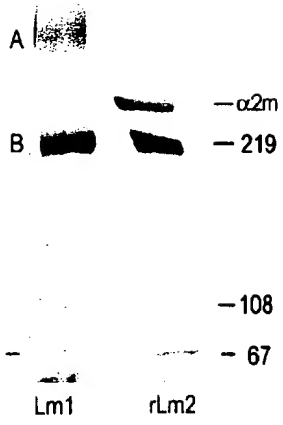


FIG. 1

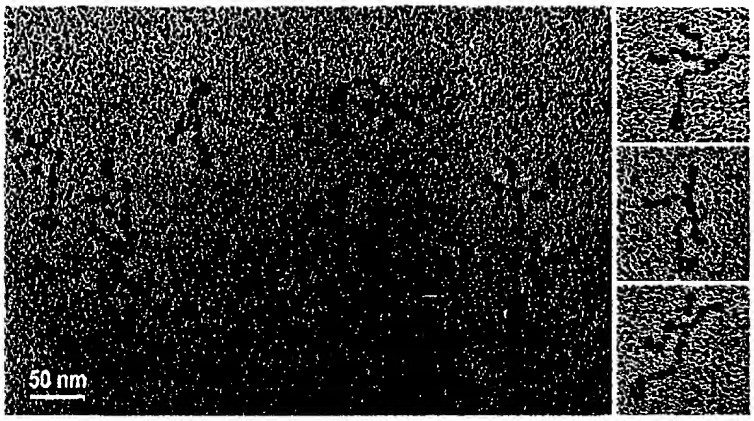


FIG. 2

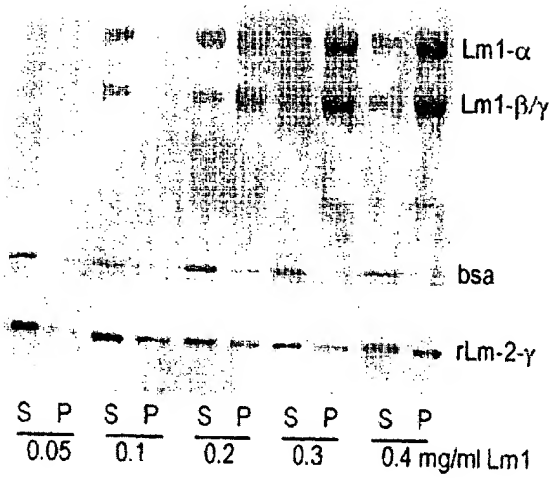
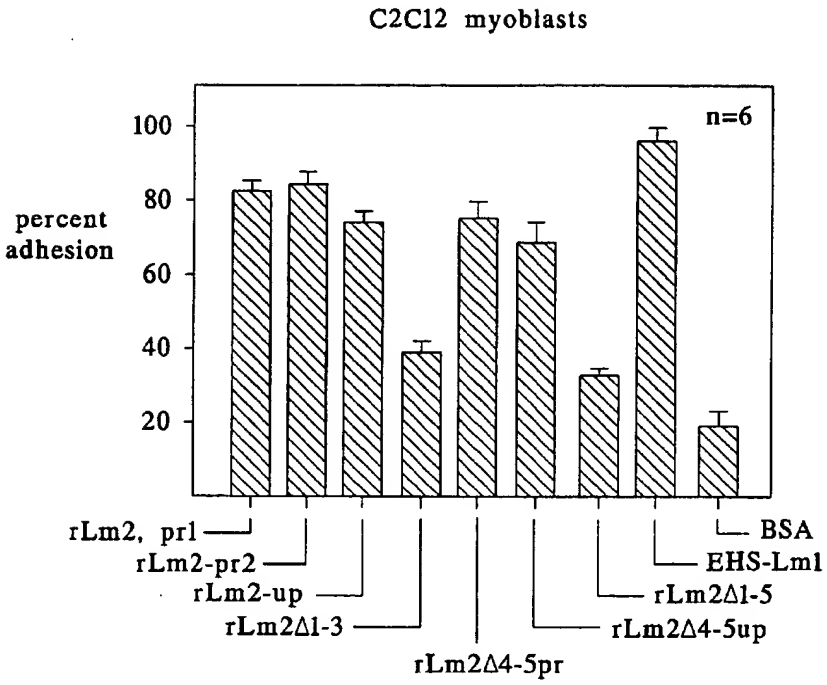


FIG.3

FIG. 4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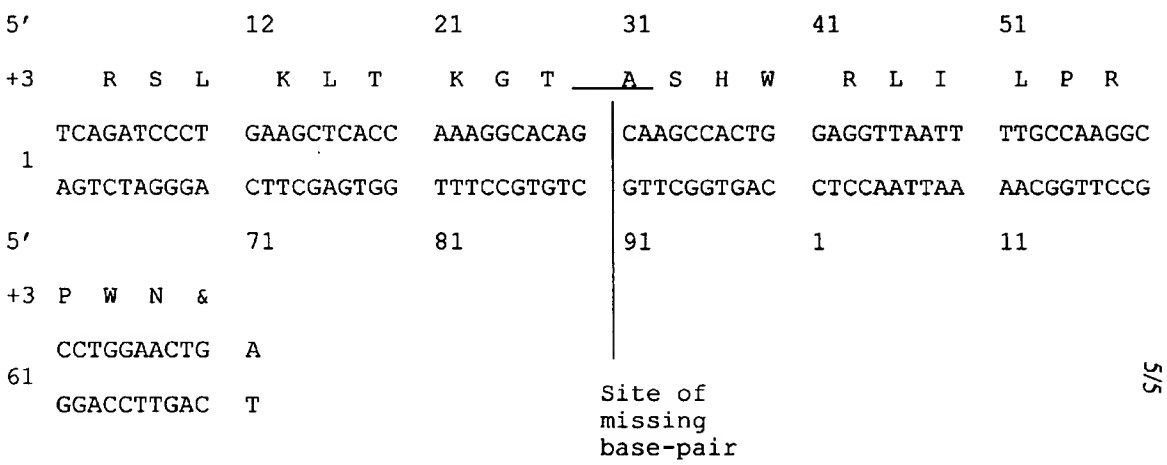
Substrate (5 μg/ml)

FIG.5



SUBSTITUTE SHEET (RULE 26)

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Gly Ser Leu Asn Glu Val Cys Val Lys Asp Glu Lys His Ala Arg Arg
420                 425                 430                 435

ggt ttg gca cct gga tcc tgt cat tgc aaa act ggt ttt gga ggt gtg   1402
Gly Leu Ala Pro Gly Ser Cys His Cys Lys Thr Gly Phe Gly Gly Val
                440                 445                 450

agc tgt gat cgg tgt gcc agg ggc tac act ggc tac ccg gac tgc aaa   1450
Ser Cys Asp Arg Cys Ala Arg Gly Tyr Thr Gly Tyr Pro Asp Cys Lys
            455                 460                 465

gcc tgt aac tgc agt ggg tta ggg agc aaa aat gag gat cct tgt ttt   1498
Ala Cys Asn Cys Ser Gly Leu Gly Ser Lys Asn Glu Asp Pro Cys Phe
        470                 475                 480

ggc ccc tgt atc tgc aag gaa aat gtt gaa gga gga gac tgt agt cgt   1546
Gly Pro Cys Ile Cys Lys Glu Asn Val Glu Gly Gly Asp Cys Ser Arg
    485                 490                 495

tgc aaa tcc ggc ttc ttc aat ttg caa gag gat aat tgg aaa ggc tgc   1594
Cys Lys Ser Gly Phe Phe Asn Leu Gln Glu Asp Asn Trp Lys Gly Cys
500                 505                 510                 515

gat gag tgt ttc tgt tca ggg gtt tca aac aga tgt cag agt tcc tac   1642
Asp Glu Cys Phe Cys Ser Gly Val Ser Asn Arg Cys Gln Ser Ser Tyr
                520                 525                 530

tgg acc tat ggc aaa ata caa gat atg agt ggc tgg tat ctg act gac   1690
Trp Thr Tyr Gly Lys Ile Gln Asp Met Ser Gly Trp Tyr Leu Thr Asp
            535                 540                 545

ctt cct ggc cgc att cga gtg gct ccc cag cag gac gac ttg gac tca   1738
Leu Pro Gly Arg Ile Arg Val Ala Pro Gln Gln Asp Asp Leu Asp Ser
        550                 555                 560

cct cag cag atc agc atc agt aac gcg gag gcc cgg caa gcc ctg ccg   1786
Pro Gln Gln Ile Ser Ile Ser Asn Ala Glu Ala Arg Gln Ala Leu Pro
    565                 570                 575

cac agc tac tac tgg agc gcg ccg gct ccc tat ctg gga aac aaa ctc   1834
His Ser Tyr Tyr Trp Ser Ala Pro Ala Pro Tyr Leu Gly Asn Lys Leu
580                 585                 590                 595

cca gca gta gga gga cag ttg aca ttt acc ata tca tat gac ctt gaa   1882
Pro Ala Val Gly Gly Gln Leu Thr Phe Thr Ile Ser Tyr Asp Leu Glu
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                600                 605                 610

gaa gag gaa gaa gat aca gaa cgt gtt ctc cag ctt atg att atc tta   1930
Glu Glu Glu Glu Asp Thr Glu Arg Val Leu Gln Leu Met Ile Ile Leu
            615                 620                 625

gag ggt aat gac ttg agc atc agc aca gcc caa gat gag gtg tac ctg   1978
Glu Gly Asn Asp Leu Ser Ile Ser Thr Ala Gln Asp Glu Val Tyr Leu
        630                 635                 640

cac cca tct gaa gaa cat act aat gta ttg tta ctt aaa gaa gaa tca   2026
His Pro Ser Glu Glu His Thr Asn Val Leu Leu Leu Lys Glu Glu Ser
    645                 650                 655

ttt acc ata cat ggc aca cat ttt cca gtc cgt aga aag gaa ttt atg   2074
Phe Thr Ile His Gly Thr His Phe Pro Val Arg Arg Lys Glu Phe Met
660                 665                 670                 675

aca gtg ctt gcg aat ttg aag aga gtc ctc cta caa atc aca tac agc   2122
Thr Val Leu Ala Asn Leu Lys Arg Val Leu Leu Gln Ile Thr Tyr Ser
                680                 685                 690

ttt ggg atg gat gcc atc ttc agg ttg agc tct gtt aac ctt gaa tcc   2170
Phe Gly Met Asp Ala Ile Phe Arg Leu Ser Ser Val Asn Leu Glu Ser
            695                 700                 705

gct gtc tcc tat cct act gat gga agc att gca gca gct gta gaa gtg   2218
Ala Val Ser Tyr Pro Thr Asp Gly Ser Ile Ala Ala Ala Val Glu Val
        710                 715                 720

tgt cag tgc cca cca ggg tat act ggc tcc tct tgt gaa tct tgt tgg   2266
Cys Gln Cys Pro Pro Gly Tyr Thr Gly Ser Ser Cys Glu Ser Cys Trp
    725                 730                 735

cct agg cac agg cga gtt aac ggc act att ttt ggt ggc atc tgt gag   2314
Pro Arg His Arg Arg Val Asn Gly Thr Ile Phe Gly Gly Ile Cys Glu
740                 745                 750                 755

cca tgt cag tgc ttt ggt cat gcg gag tcc tgt gat gac gtc act gga   2362
Pro Cys Gln Cys Phe Gly His Ala Glu Ser Cys Asp Asp Val Thr Gly
                760                 765                 770

gaa tgc ctg aac tgt aag gat cac aca ggt ggc cca tat tgt gat aaa   2410
Glu Cys Leu Asn Cys Lys Asp His Thr Gly Gly Pro Tyr Cys Asp Lys
            775                 780                 785

tgt ctt cct ggt ttc tat ggc gag cct act aaa gga acc tct gaa gac   2458
Cys Leu Pro Gly Phe Tyr Gly Glu Pro Thr Lys Gly Thr Ser Glu Asp
        790                 795                 800

tgt caa ccc tgt gcc tgt cca ctc aat atc cca tcc aat aac ttt agc   2506
Cys Gln Pro Cys Ala Cys Pro Leu Asn Ile Pro Ser Asn Asn Phe Ser
    805                 810                 815

cca acg tgc cat tta gac cgg agt ctt gga ttg atc tgt gat gga tgc   2554
Pro Thr Cys His Leu Asp Arg Ser Leu Gly Leu Ile Cys Asp Gly Cys
820                 825                 830                 835

cct gtc ggg tac aca gga cca cgc tgt gag agg tgt gca gaa ggc tat   2602
Pro Val Gly Tyr Thr Gly Pro Arg Cys Glu Arg Cys Ala Glu Gly Tyr
                840                 845                 850
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ttt gga caa ccc tct gta cct gga gga tca tgt cag cca tgc caa tgc   2650
Phe Gly Gln Pro Ser Val Pro Gly Gly Ser Cys Gln Pro Cys Gln Cys
            855                 860                 865

aat gac aac ctt gac ttc tcc atc cct ggc agc tgt gac agc ttg tct   2698
Asn Asp Asn Leu Asp Phe Ser Ile Pro Gly Ser Cys Asp Ser Leu Ser
        870                 875                 880

ggc tcc tgt ctg ata tgt aaa cca ggt aca aca ggc cgg tac tgt gag   2746
Gly Ser Cys Leu Ile Cys Lys Pro Gly Thr Thr Gly Arg Tyr Cys Glu
    885                 890                 895

ctc tgt gct gat gga tat ttt gga gat gca gtt gat gcg aag aac tgt   2794
Leu Cys Ala Asp Gly Tyr Phe Gly Asp Ala Val Asp Ala Lys Asn Cys
900                 905                 910                 915

cag ccc tgt cgc tgt aat gcc ggt ggc tct ttc tct gag gtt tgc cac   2842
Gln Pro Cys Arg Cys Asn Ala Gly Gly Ser Phe Ser Glu Val Cys His
                920                 925                 930

agt caa act gga cag tgt gag tgc aga gcc aac gtt cag ggt cag aga   2890
Ser Gln Thr Gly Gln Cys Glu Cys Arg Ala Asn Val Gln Gly Gln Arg
            935                 940                 945

tgt gac aaa tgc aag gct ggg acc ttt ggc cta caa tca gca agg ggc   2938
Cys Asp Lys Cys Lys Ala Gly Thr Phe Gly Leu Gln Ser Ala Arg Gly
        950                 955                 960

tgt gtt ccc tgc aac tgc aat tct ttt ggg tct aag tca ttc gac tgt   2986
Cys Val Pro Cys Asn Cys Asn Ser Phe Gly Ser Lys Ser Phe Asp Cys
    965                 970                 975

gaa gag agt gga caa tgt tgg tgc caa cct gga gtc aca ggg aag aaa   3034
Glu Glu Ser Gly Gln Cys Trp Cys Gln Pro Gly Val Thr Gly Lys Lys
980                 985                 990                 995

tgt gac cgc tgt gcc cac ggc tat ttc aac ttc caa gaa gga ggc tgc   3082
Cys Asp Arg Cys Ala His Gly Tyr Phe Asn Phe Gln Glu Gly Gly Cys
                1000                1005                1010

aca gct tgt gaa tgt tct cat ctg ggt aat aat tgt gac cca aag act   3130
Thr Ala Cys Glu Cys Ser His Leu Gly Asn Asn Cys Asp Pro Lys Thr
            1015                1020                1025

ggg cga tgc att tgc cca ccc aat acc att gga gag aaa tgt tct aaa   3178
Gly Arg Cys Ile Cys Pro Pro Asn Thr Ile Gly Glu Lys Cys Ser Lys
        1030                1035                1040

tgt gca ccc aat acc tgg ggc cac agc att acc act ggt tgt aag gct   3226
Cys Ala Pro Asn Thr Trp Gly His Ser Ile Thr Thr Gly Cys Lys Ala
    1045                1050                1055

tgt aac tgc agc aca gtg gga tcc ttg gat ttc caa tgc aat gta aat   3274
Cys Asn Cys Ser Thr Val Gly Ser Leu Asp Phe Gln Cys Asn Val Asn
1060                1065                1070                1075

aca ggc caa tgc aac tgt cat cca aaa ttc tct ggt gca aaa tgt aca   3322
Thr Gly Gln Cys Asn Cys His Pro Lys Phe Ser Gly Ala Lys Cys Thr
                1080                1085                1090
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gag tgc agt cga ggt cac tgg aac tac cct cgc tgc aat ctc tgt gac   3370
Glu Cys Ser Arg Gly His Trp Asn Tyr Pro Arg Cys Asn Leu Cys Asp
          1095                1100                1105

tgc ttc ctc cct ggg aca gat gcc aca acc tgt gat tca gag act aaa   3418
Cys Phe Leu Pro Gly Thr Asp Ala Thr Thr Cys Asp Ser Glu Thr Lys
     1110                1115                1120

aaa tgc tcc tgt agt gat caa act ggg cag tgc act tgt aag gtg aat   3466
Lys Cys Ser Cys Ser Asp Gln Thr Gly Gln Cys Thr Cys Lys Val Asn
   1125                1130                1135

gtg gaa ggc atc cac tgt gac aga tgc cgg cct ggc aaa ttc gga ctc   3514
Val Glu Gly Ile His Cys Asp Arg Cys Arg Pro Gly Lys Phe Gly Leu
1140                1145                1150                1155

gat gcc aag aat cca ctt ggc tgc agc agc tgc tat tgc ttc ggc act   3562
Asp Ala Lys Asn Pro Leu Gly Cys Ser Ser Cys Tyr Cys Phe Gly Thr
               1160                1165                1170

act acc cag tgc tct gaa gca aaa gga ctg atc cgg acg tgg gtg act   3610
Thr Thr Gln Cys Ser Glu Ala Lys Gly Leu Ile Arg Thr Trp Val Thr
          1175                1180                1185

ctg aag gct gag cag acc att cta ccc ctg gta gat gag gct ctg cag   3658
Leu Lys Ala Glu Gln Thr Ile Leu Pro Leu Val Asp Glu Ala Leu Gln
       1190                1195                1200

cac acg acc acc aag ggc att gtt ttt caa cat cca gag att gtt gcc   3706
His Thr Thr Thr Lys Gly Ile Val Phe Gln His Pro Glu Ile Val Ala
   1205                1210                1215

cac atg gac ctg atg aga gaa gat ctc cat ttg gaa cct ttt tat tgg   3754
His Met Asp Leu Met Arg Glu Asp Leu His Leu Glu Pro Phe Tyr Trp
1220                1225                1230                1235

aaa ctt cca gaa caa ttt gaa gga aag aag ttg atg gcc tat ggg ggc   3802
Lys Leu Pro Glu Gln Phe Glu Gly Lys Lys Leu Met Ala Tyr Gly Gly
               1240                1245                1250

aaa ctc aag tat gca atc tat ttc gag gct cgg gaa gaa aca ggt ttc   3850
Lys Leu Lys Tyr Ala Ile Tyr Phe Glu Ala Arg Glu Glu Thr Gly Phe
          1255                1260                1265

tct aca tat aat cct caa gtg atc att cga ggt ggg aca cct act cat   3898
Ser Thr Tyr Asn Pro Gln Val Ile Ile Arg Gly Gly Thr Pro Thr His
       1270                1275                1280

gct aga att atc gtc agg cat atg gct gct cct ctg att ggc caa ttg   3946
Ala Arg Ile Ile Val Arg His Met Ala Ala Pro Leu Ile Gly Gln Leu
   1285                1290                1295

aca agg cat gaa att gaa atg aca gag aaa gaa tgg aaa tat tat ggg   3994
Thr Arg His Glu Ile Glu Met Thr Glu Lys Glu Trp Lys Tyr Tyr Gly
1300                1305                1310                1315

gat gat cct cga gtc cat aga act gtg acc cga gaa gac ttc ttg gat   4042
Asp Asp Pro Arg Val His Arg Thr Val Thr Arg Glu Asp Phe Leu Asp
               1320                1325                1330

ata cta tat gat att cat tac att ctt atc aaa gct act tat gga aat   4090
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Ile Leu Tyr Asp Ile His Tyr Ile Leu Ile Lys Ala Thr Tyr Gly Asn
          1335                1340                1345

ttc atg cga caa agc agg att tct gaa atc tca atg gag gta gct gaa   4138
Phe Met Arg Gln Ser Arg Ile Ser Glu Ile Ser Met Glu Val Ala Glu
       1350                1355                1360

caa gga cgt gga aca aca atg act cct cca gct gac ttg att gaa aaa   4186
Gln Gly Arg Gly Thr Thr Met Thr Pro Pro Ala Asp Leu Ile Glu Lys
   1365                1370                1375

tgt gat tgt ccc ctg ggc tat tct ggc ctg tcc tgt gag gca tgc ttg   4234
Cys Asp Cys Pro Leu Gly Tyr Ser Gly Leu Ser Cys Glu Ala Cys Leu
1380                1385                1390                1395

ccg gga ttt tat cga ctg cgt tct caa cca ggt ggc cgc acc cct gga   4282
Pro Gly Phe Tyr Arg Leu Arg Ser Gln Pro Gly Gly Arg Thr Pro Gly
               1400                1405                1410

cca acc ctg ggc acc tgt gtt cca tgt caa tgt aat gga cac agc agc   4330
Pro Thr Leu Gly Thr Cys Val Pro Cys Gln Cys Asn Gly His Ser Ser
          1415                1420                1425

ctg tgt gac cct gaa aca tcg ata tgc cag aat tgt caa cat cac act   4378
Leu Cys Asp Pro Glu Thr Ser Ile Cys Gln Asn Cys Gln His His Thr
       1430                1435                1440

gct ggt gac ttc tgt gaa cga tgt gct ctt gga tac tat gga att gtc   4426
Ala Gly Asp Phe Cys Glu Arg Cys Ala Leu Gly Tyr Tyr Gly Ile Val
   1445                1450                1455

aag gga ttg cca aat gac tgt cag caa tgt gcc tgc cct ctg att tct   4474
Lys Gly Leu Pro Asn Asp Cys Gln Gln Cys Ala Cys Pro Leu Ile Ser
1460                1465                1470                1475

tcc agt aac aat ttc agc ccc tct tgt gtc gca gaa gga ctt gac gac   4522
Ser Ser Asn Asn Phe Ser Pro Ser Cys Val Ala Glu Gly Leu Asp Asp
               1480                1485                1490

tac cgc tgc acg gct tgt cca cgg gga tat gaa ggc cag tac tgt gaa   4570
Tyr Arg Cys Thr Ala Cys Pro Arg Gly Tyr Glu Gly Gln Tyr Cys Glu
          1495                1500                1505

agg tgt gcc cct ggc tat act ggc agt cca ggc aac cct gga ggc tcc   4618
Arg Cys Ala Pro Gly Tyr Thr Gly Ser Pro Gly Asn Pro Gly Gly Ser
       1510                1515                1520

tgc caa gaa tgt gag tgt gat ccc tat ggc tca ctg cct gtg ccc tgt   4666
Cys Gln Glu Cys Glu Cys Asp Pro Tyr Gly Ser Leu Pro Val Pro Cys
   1525                1530                1535

gac cct gtc aca gga ttc tgc acg tgc cga cct gga gcc acg gga agg   4714
Asp Pro Val Thr Gly Phe Cys Thr Cys Arg Pro Gly Ala Thr Gly Arg
1540                1545                1550                1555

aag tgt gac ggc tgc aag cac tgg cat gca cgc gag ggc tgg gag tgt   4762
Lys Cys Asp Gly Cys Lys His Trp His Ala Arg Glu Gly Trp Glu Cys
               1560                1565                1570

gtt ttt tgt gga gat gag tgc act ggc ctt ctt ctc ggt gac ttg gct   4810
Val Phe Cys Gly Asp Glu Cys Thr Gly Leu Leu Leu Gly Asp Leu Ala
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          1575                1580                1585

cgc ctg gag cag atg gtc atg agc atc aac ctc act ggt ccg ctg cct   4858
Arg Leu Glu Gln Met Val Met Ser Ile Asn Leu Thr Gly Pro Leu Pro
       1590                1595                1600

gcg cca tat aaa atg ctg tat ggt ctt gaa aat atg act cag gag cta   4906
Ala Pro Tyr Lys Met Leu Tyr Gly Leu Glu Asn Met Thr Gln Glu Leu
   1605                1610                1615

aag cac ttg ctg tca cct cag cgg gcc cca gag agg ctt att cag ctg   4954
Lys His Leu Leu Ser Pro Gln Arg Ala Pro Glu Arg Leu Ile Gln Leu
1620                1625                1630                1635

gca gag ggc aat ctg aat aca ctc gtg acc gaa atg aac gag ctg ctg   5002
Ala Glu Gly Asn Leu Asn Thr Leu Val Thr Glu Met Asn Glu Leu Leu
               1640                1645                1650

acc agg gct acc aaa gtg aca gca gat ggc gag cag acc gga cag gat   5050
Thr Arg Ala Thr Lys Val Thr Ala Asp Gly Glu Gln Thr Gly Gln Asp
          1655                1660                1665

gct gag agg acc aac aca aga gca aag tcc ctg gga gaa ttc att aag   5098
Ala Glu Arg Thr Asn Thr Arg Ala Lys Ser Leu Gly Glu Phe Ile Lys
       1670                1675                1680

gag ctt gcc cgg gat gca gaa gct gta aat gaa aaa gct ata aaa cta   5146
Glu Leu Ala Arg Asp Ala Glu Ala Val Asn Glu Lys Ala Ile Lys Leu
   1685                1690                1695

aat gaa act cta gga act cga gac gag gcc ttt gag aga aat ttg gaa   5194
Asn Glu Thr Leu Gly Thr Arg Asp Glu Ala Phe Glu Arg Asn Leu Glu
1700                1705                1710                1715

ggg ctt cag aaa gag att gac cag atg att aaa gaa ctg agg agg aaa   5242
Gly Leu Gln Lys Glu Ile Asp Gln Met Ile Lys Glu Leu Arg Arg Lys
               1720                1725                1730

aat cta gag aca caa aag gaa att gct gaa gat gag ttg gta gct gca   5290
Asn Leu Glu Thr Gln Lys Glu Ile Ala Glu Asp Glu Leu Val Ala Ala
          1735                1740                1745

gaa gcc ctt ctg aaa aaa gtg aag aag ctg ttt gga gag tcc cgg ggg   5338
Glu Ala Leu Leu Lys Lys Val Lys Lys Leu Phe Gly Glu Ser Arg Gly
       1750                1755                1760

gaa aat gaa gaa atg gag aag gat ctc cgg gaa aaa ctg gct gac tac   5386
Glu Asn Glu Glu Met Glu Lys Asp Leu Arg Glu Lys Leu Ala Asp Tyr
   1765                1770                1775

aaa aac aaa gtt gat gat gct tgg gac ctt ttg aga gaa gcc aca gat   5434
Lys Asn Lys Val Asp Asp Ala Trp Asp Leu Leu Arg Glu Ala Thr Asp
1780                1785                1790                1795

aaa atc aga gaa gct aat cgc cta ttt gca gta aat cag aaa aac atg   5482
Lys Ile Arg Glu Ala Asn Arg Leu Phe Ala Val Asn Gln Lys Asn Met
               1800                1805                1810

act gca ttg gag aaa aag aag gag gct gtt gag agc ggc aaa cga caa   5530
Thr Ala Leu Glu Lys Lys Lys Glu Ala Val Glu Ser Gly Lys Arg Gln
          1815                1820                1825
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att gag aac act tta aaa gaa ggc aat gac ata ctc gat gaa gcc aac   5578
Ile Glu Asn Thr Leu Lys Glu Gly Asn Asp Ile Leu Asp Glu Ala Asn
       1830                1835                1840

cgt ctt gca gat gaa atc aac tcc atc ata gac tat gtt gaa gac atc   5626
Arg Leu Ala Asp Glu Ile Asn Ser Ile Ile Asp Tyr Val Glu Asp Ile
   1845                1850                1855

caa act aaa ttg cca cct atg tct gag gag ctt aat gat aaa ata gat   5674
Gln Thr Lys Leu Pro Pro Met Ser Glu Glu Leu Asn Asp Lys Ile Asp
1860                1865                1870                1875

gac ctc tcc caa gaa ata aag gac agg aag ctt gct gag aag gtg tcc   5722
Asp Leu Ser Gln Glu Ile Lys Asp Arg Lys Leu Ala Glu Lys Val Ser
             1880                1885                1890

cag gct gag agc cac gca gct cag ttg aat gac tca tct gct gtc ctt   5770
Gln Ala Glu Ser His Ala Ala Gln Leu Asn Asp Ser Ser Ala Val Leu
          1895                1900                1905

gat gga atc ctt gat gag gct aaa aac atc tcc ttc aat gcc act gca   5818
Asp Gly Ile Leu Asp Glu Ala Lys Asn Ile Ser Phe Asn Ala Thr Ala
       1910                1915                1920

gcc ttc aaa gct tac agc aat att aag gac tat att gat gaa gct gag   5866
Ala Phe Lys Ala Tyr Ser Asn Ile Lys Asp Tyr Ile Asp Glu Ala Glu
   1925                1930                1935

aaa gtt gcc aaa gaa gcc aaa gat ctt gca cat gaa gct aca aaa ctg   5914
Lys Val Ala Lys Glu Ala Lys Asp Leu Ala His Glu Ala Thr Lys Leu
1940                1945                1950                1955

gca aca ggt cct cgg ggt tta tta aag gaa gat gcc aaa ggc tgt ctt   5962
Ala Thr Gly Pro Arg Gly Leu Leu Lys Glu Asp Ala Lys Gly Cys Leu
             1960                1965                1970

cag aaa agc ttc agg att ctt aac gaa gcc aag aag tta gca aat gat   6010
Gln Lys Ser Phe Arg Ile Leu Asn Glu Ala Lys Lys Leu Ala Asn Asp
          1975                1980                1985

gta aaa gaa aat gaa gac cat cta aat ggc tta aaa acc agg ata gaa   6058
Val Lys Glu Asn Glu Asp His Leu Asn Gly Leu Lys Thr Arg Ile Glu
       1990                1995                2000

aat gct gat gct aga aat ggg gat ctc ttg aga act ttg aat gac act   6106
Asn Ala Asp Ala Arg Asn Gly Asp Leu Leu Arg Thr Leu Asn Asp Thr
   2005                2010                2015

ttg gga aag tta tca gct att cca aat gat aca gct gct aaa ctg caa   6154
Leu Gly Lys Leu Ser Ala Ile Pro Asn Asp Thr Ala Ala Lys Leu Gln
2020                2025                2030                2035

gct gtt aag gac aaa gcc aga caa gcc aac gac aca gct aaa gat gta   6202
Ala Val Lys Asp Lys Ala Arg Gln Ala Asn Asp Thr Ala Lys Asp Val
             2040                2045                2050

ctg gca cag att aca gag ctc cac cag aac ctc gat ggc ctg aag aag   6250
Leu Ala Gln Ile Thr Glu Leu His Gln Asn Leu Asp Gly Leu Lys Lys
          2055                2060                2065
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aat tac aat aaa cta gca gac agc gtc gcc aaa acg aat gct gtg gtt   6298
Asn Tyr Asn Lys Leu Ala Asp Ser Val Ala Lys Thr Asn Ala Val Val
       2070                2075                2080

aaa gat cct tcc aag aac aaa atc att gcc gat gca gat gcc act gtc   6346
Lys Asp Pro Ser Lys Asn Lys Ile Ile Ala Asp Ala Asp Ala Thr Val
   2085                2090                2095

aaa aat tta gaa cag gaa gct gac cgg cta ata gat aaa ctc aaa ccc   6394
Lys Asn Leu Glu Gln Glu Ala Asp Arg Leu Ile Asp Lys Leu Lys Pro
2100                2105                2110                2115

atc aag gaa ctt gag gat aac cta aag aaa aac atc tct gag ata aag   6442
Ile Lys Glu Leu Glu Asp Asn Leu Lys Lys Asn Ile Ser Glu Ile Lys
                2120                2125                2130

gaa ttg ata aac caa gct cgg aaa caa gcc aat tct atc aaa gta tct   6490
Glu Leu Ile Asn Gln Ala Arg Lys Gln Ala Asn Ser Ile Lys Val Ser
           2135                2140                2145

gtg tct tca gga ggt gac tgc att cga aca tac aaa cca gaa atc aag   6538
Val Ser Ser Gly Gly Asp Cys Ile Arg Thr Tyr Lys Pro Glu Ile Lys
       2150                2155                2160

aaa gga agt tac aat aat att gtt gtc aac gta aag aca gct gtt gct   6586
Lys Gly Ser Tyr Asn Asn Ile Val Val Asn Val Lys Thr Ala Val Ala
   2165                2170                2175

gat aac ctc ctc ttt tat ctt gga agt gcc aaa ttt att gac ttt ctg   6634
Asp Asn Leu Leu Phe Tyr Leu Gly Ser Ala Lys Phe Ile Asp Phe Leu
2180                2185                2190                2195

gct ata gaa atg cgt aaa ggc aaa gtc agc ttc ctc tgg gat gtt gga   6682
Ala Ile Glu Met Arg Lys Gly Lys Val Ser Phe Leu Trp Asp Val Gly
                2200                2205                2210

tct gga gtt gga cgt gta gag tac cca gat ttg act att gat gac tca   6730
Ser Gly Val Gly Arg Val Glu Tyr Pro Asp Leu Thr Ile Asp Asp Ser
           2215                2220                2225

tat tgg tac cgt atc gta gca tca aga act ggg aga aat gga act att   6778
Tyr Trp Tyr Arg Ile Val Ala Ser Arg Thr Gly Arg Asn Gly Thr Ile
       2230                2235                2240

tct gtg aga gcc ctg gat gga ccc aaa gcc agc att gtg ccc agc aca   6826
Ser Val Arg Ala Leu Asp Gly Pro Lys Ala Ser Ile Val Pro Ser Thr
   2245                2250                2255

cac cat tcg acg tct cct cca ggg tac acg att cta gat gtg gat gca   6874
His His Ser Thr Ser Pro Pro Gly Tyr Thr Ile Leu Asp Val Asp Ala
2260                2265                2270                2275

aat gca atg ctg ttt gtt ggt ggc ctg act ggg aaa tta aag aag gct   6922
Asn Ala Met Leu Phe Val Gly Gly Leu Thr Gly Lys Leu Lys Lys Ala
                2280                2285                2290

gat gct gta cgt gtg att aca ttc act ggc tgc atg gga gaa aca tac   6970
Asp Ala Val Arg Val Ile Thr Phe Thr Gly Cys Met Gly Glu Thr Tyr
           2295                2300                2305

ttt gac aac aaa cct ata ggt ttg tgg aat ttc cga gaa aaa gaa ggt   7018
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Phe Asp Asn Lys Pro Ile Gly Leu Trp Asn Phe Arg Glu Lys Glu Gly
       2310                2315                2320

gac tgc aaa gga tgc act gtc agt cct cag gtg gaa gat agt gag ggg   7066
Asp Cys Lys Gly Cys Thr Val Ser Pro Gln Val Glu Asp Ser Glu Gly
   2325                2330                2335

act att caa ttt gat gga gaa ggt tat gca ttg gtc agc cgt ccc att   7114
Thr Ile Gln Phe Asp Gly Glu Gly Tyr Ala Leu Val Ser Arg Pro Ile
2340                2345                2350                2355

cgc tgg tac ccc aac atc tcc act gtc atg ttc aag ttc aga aca ttt   7162
Arg Trp Tyr Pro Asn Ile Ser Thr Val Met Phe Lys Phe Arg Thr Phe
               2360                2365                2370

tct tcg agt gct ctt ctg atg tat ctt gcc aca cga gac ctg aga gat   7210
Ser Ser Ser Ala Leu Leu Met Tyr Leu Ala Thr Arg Asp Leu Arg Asp
           2375                2380                2385

ttc atg agt gtg gag ctc act gat ggg cac ata aaa gtc agt tac gat   7258
Phe Met Ser Val Glu Leu Thr Asp Gly His Ile Lys Val Ser Tyr Asp
       2390                2395                2400

ctg ggc tca gga atg gct tcc gtt gtc agc aat caa aac cat aat gat   7306
Leu Gly Ser Gly Met Ala Ser Val Val Ser Asn Gln Asn His Asn Asp
   2405                2410                2415

ggg aaa tgg aaa tca ttc act ctg tca aga att caa aaa caa gcc aat   7354
Gly Lys Trp Lys Ser Phe Thr Leu Ser Arg Ile Gln Lys Gln Ala Asn
2420                2425                2430                2435

ata tca att gta gat ata gat act aat cag gag gag aat ata gca act   7402
Ile Ser Ile Val Asp Ile Asp Thr Asn Gln Glu Glu Asn Ile Ala Thr
               2440                2445                2450

tcg tct tct gga aac aac ttt ggt ctt gac ttg aaa gca gat gac aaa   7450
Ser Ser Ser Gly Asn Asn Phe Gly Leu Asp Leu Lys Ala Asp Asp Lys
           2455                2460                2465

ata tat ttt ggt ggc ctg cca acg ctg aga aac ttg agt atg aaa gca   7498
Ile Tyr Phe Gly Gly Leu Pro Thr Leu Arg Asn Leu Ser Met Lys Ala
       2470                2475                2480

agg cca gaa gta aat ctg aag aaa tat tcc ggc tgc ctc aaa gat att   7546
Arg Pro Glu Val Asn Leu Lys Lys Tyr Ser Gly Cys Leu Lys Asp Ile
   2485                2490                2495

gaa att tca aga act ccg tac aat ata ctc agt agt ccc gat tat gtt   7594
Glu Ile Ser Arg Thr Pro Tyr Asn Ile Leu Ser Ser Pro Asp Tyr Val
2500                2505                2510                2515

ggt gtt acc aaa gga tgt tcc ctg gag aat gtt tac aca gtt agc ttt   7642
Gly Val Thr Lys Gly Cys Ser Leu Glu Asn Val Tyr Thr Val Ser Phe
               2520                2525                2530

cct aag cct ggt ttt gtg gag ctc tcc cct gtg cca att gat gta gga   7690
Pro Lys Pro Gly Phe Val Glu Leu Ser Pro Val Pro Ile Asp Val Gly
           2535                2540                2545

aca gaa atc aac ctg tca ttc agc acc aag aat gag tcc ggc atc att   7738
Thr Glu Ile Asn Leu Ser Phe Ser Thr Lys Asn Glu Ser Gly Ile Ile
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      2550                2555                2560

ctt ttg gga agt gga ggg aca cca gca cca cct agg aga aaa cga agg   7786
Leu Leu Gly Ser Gly Gly Thr Pro Ala Pro Pro Arg Arg Lys Arg Arg
   2565                2570                2575

cag act gga cag gcc tat tat gta ata ctc ctc aac agg ggc cgt ctg   7834
Gln Thr Gly Gln Ala Tyr Tyr Val Ile Leu Leu Asn Arg Gly Arg Leu
2580                2585                2590                2595

gaa gtg cat ctc tcc aca ggg gca cga aca atg agg aaa att gtc atc   7882
Glu Val His Leu Ser Thr Gly Ala Arg Thr Met Arg Lys Ile Val Ile
                2600                2605                2610

aga cca gag ccg aat ctg ttt cat gat gga aga gaa cat tcc gtt cat   7930
Arg Pro Glu Pro Asn Leu Phe His Asp Gly Arg Glu His Ser Val His
          2615                2620                2625

gta gag cga act aga ggc atc ttt aca gtt caa gtg gat gaa aac aga   7978
Val Glu Arg Thr Arg Gly Ile Phe Thr Val Gln Val Asp Glu Asn Arg
       2630                2635                2640

aga tac atg caa aac ctg aca gtt gaa cag cct atc gaa gtt aaa aag   8026
Arg Tyr Met Gln Asn Leu Thr Val Glu Gln Pro Ile Glu Val Lys Lys
   2645                2650                2655

ctt ttc gtt ggg ggt gct cca cct gaa ttt caa cct tcc cca ctc aga   8074
Leu Phe Val Gly Gly Ala Pro Pro Glu Phe Gln Pro Ser Pro Leu Arg
2660                2665                2670                2675

aat att cct cct ttt gaa ggc tgc ata tgg aat ctt gtt att aac tct   8122
Asn Ile Pro Pro Phe Glu Gly Cys Ile Trp Asn Leu Val Ile Asn Ser
                2680                2685                2690

gtc ccc atg gac ttt gca agg cct gtg tcc ttc aaa aat gct gac att   8170
Val Pro Met Asp Phe Ala Arg Pro Val Ser Phe Lys Asn Ala Asp Ile
          2695                2700                2705

ggt cgc tgt gcc cat cag aaa ctc cgt gaa gat gaa gat gga gca gct   8218
Gly Arg Cys Ala His Gln Lys Leu Arg Glu Asp Glu Asp Gly Ala Ala
       2710                2715                2720

cca gct gaa ata gtt atc cag cct gag cca gtt ccc acc cca gcc ttt   8266
Pro Ala Glu Ile Val Ile Gln Pro Glu Pro Val Pro Thr Pro Ala Phe
   2725                2730                2735

cct acg ccc acc cca gtt ctg aca cat ggt cct tgt gct gca gaa tca   8314
Pro Thr Pro Thr Pro Val Leu Thr His Gly Pro Cys Ala Ala Glu Ser
2740                2745                2750                2755

gaa cca gct ctt ttg ata ggg agc aag cag ttc ggg ctt tca aga aac   8362
Glu Pro Ala Leu Leu Ile Gly Ser Lys Gln Phe Gly Leu Ser Arg Asn
                2760                2765                2770

agt cac att gca att gca ttt gat gac acc aaa gtt aaa aac cgt ctc   8410
Ser His Ile Ala Ile Ala Phe Asp Asp Thr Lys Val Lys Asn Arg Leu
          2775                2780                2785

aca att gag ttg gaa gta aga acc gaa gct gaa tcc ggc ttg ctt ttt   8458
Thr Ile Glu Leu Glu Val Arg Thr Glu Ala Glu Ser Gly Leu Leu Phe
       2790                2795                2800
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tac atg gct gcg atc aat cat gct gat ttt gca aca gtt cag ctg aga   8506
Tyr Met Ala Ala Ile Asn His Ala Asp Phe Ala Thr Val Gln Leu Arg
   2805                2810                2815

aat gga ttg ccc tac ttc agc tat gac ttg ggg agt ggg gac acc cac   8554
Asn Gly Leu Pro Tyr Phe Ser Tyr Asp Leu Gly Ser Gly Asp Thr His
2820                2825                2830                2835

acc atg atc ccc acc aaa atc aat gat ggc cag tgg cac aag att aag   8602
Thr Met Ile Pro Thr Lys Ile Asn Asp Gly Gln Trp His Lys Ile Lys
              2840                2845                2850

ata atg aga agt aag caa gaa gga att ctt tat gta gat ggg gct tcc   8650
Ile Met Arg Ser Lys Gln Glu Gly Ile Leu Tyr Val Asp Gly Ala Ser
          2855                2860                2865

aac aga acc atc agt ccc aaa aaa gcc gac atc ctg gat gtc gtg gga   8698
Asn Arg Thr Ile Ser Pro Lys Lys Ala Asp Ile Leu Asp Val Val Gly
       2870                2875                2880

atg ctg tat gtt ggt ggg tta ccc atc aac tac act acc cga aga att   8746
Met Leu Tyr Val Gly Gly Leu Pro Ile Asn Tyr Thr Thr Arg Arg Ile
   2885                2890                2895

ggt cca gtg acc tat agc att gat ggc tgc gtc agg aat ctc cac atg   8794
Gly Pro Val Thr Tyr Ser Ile Asp Gly Cys Val Arg Asn Leu His Met
2900                2905                2910                2915

gca gag gcc cct gcc gat ctg gaa caa ccc acc tcc agc ttc cat gtt   8842
Ala Glu Ala Pro Ala Asp Leu Glu Gln Pro Thr Ser Ser Phe His Val
              2920                2925                2930

ggg aca tgt ttt gca aat gct cag agg gga aca tat ttt gac gga acc   8890
Gly Thr Cys Phe Ala Asn Ala Gln Arg Gly Thr Tyr Phe Asp Gly Thr
          2935                2940                2945

ggt ttt gcc aaa gca gtt ggt gga ttc aaa gtg gga ttg gac ctt ctt   8938
Gly Phe Ala Lys Ala Val Gly Gly Phe Lys Val Gly Leu Asp Leu Leu
       2950                2955                2960

gta gaa ttt gaa ttc gcg aca act aca acg act gga gtt ctt ctg ggg   8986
Val Glu Phe Glu Phe Ala Thr Thr Thr Thr Thr Gly Val Leu Leu Gly
   2965                2970                2975

atc agt agt caa aaa atg gat gga atg ggt att gaa atg att gat gaa   9034
Ile Ser Ser Gln Lys Met Asp Gly Met Gly Ile Glu Met Ile Asp Glu
2980                2985                2990                2995

aag ttg atg ttt cat gtg gac aat ggt gcg ggc aga ttc act gct gtc   9082
Lys Leu Met Phe His Val Asp Asn Gly Ala Gly Arg Phe Thr Ala Val
              3000                3005                3010

tat gat gct ggg gtt cca ggg cat ttg tgt gat gga caa tgg cat aaa   9130
Tyr Asp Ala Gly Val Pro Gly His Leu Cys Asp Gly Gln Trp His Lys
          3015                3020                3025

gtc act gcc aac aag atc aaa cac cgc att gag ctc aca gtc gat ggg   9178
Val Thr Ala Asn Lys Ile Lys His Arg Ile Glu Leu Thr Val Asp Gly
       3030                3035                3040
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aac cag gtg gaa gcc caa agc cca aac cca gca tct aca tca gct gac   9226
Asn Gln Val Glu Ala Gln Ser Pro Asn Pro Ala Ser Thr Ser Ala Asp
   3045                3050                3055

aca aat gac cct gtg ttt gtt gga ggc ttc cca gat gac ctc aag cag   9274
Thr Asn Asp Pro Val Phe Val Gly Gly Phe Pro Asp Asp Leu Lys Gln
3060                3065                3070                3075

ttt ggc cta aca acc agt att ccg ttc cga ggt tgc atc aga tcc ctg   9322
Phe Gly Leu Thr Thr Ser Ile Pro Phe Arg Gly Cys Ile Arg Ser Leu
               3080                3085                3090

aag ctc acc aaa ggc aca ggc aag cca ctg gag gtt aat ttt gcc aag   9370
Lys Leu Thr Lys Gly Thr Gly Lys Pro Leu Glu Val Asn Phe Ala Lys
          3095                3100                3105

gcc ctg gaa ctgaggggcg ttcaacctgt atcatgccca gccaactaat           9419
Ala Leu Glu
       3110

aaaaataagt gtaaccccag gaagagtctg tcaaaacaag tatatcaagt aaaacaaaca 9479

aatatatttt acctatatat gttaattaaa ctaatttgtg catgtacata gaattc     9535


<210> 2
<211> 3110
<212> PRT
<213> Homo sapiens

<400> 2
Met Pro Gly Ala Ala Gly Val Leu Leu Leu Leu Leu Leu Ser Gly Gly
  1               5                  10                  15

Leu Gly Gly Val Gln Ala Gln Arg Pro Gln Gln Gln Arg Gln Ser Gln
             20                  25                  30

Ala His Gln Gln Arg Gly Leu Phe Pro Ala Val Leu Asn Leu Ala Ser
         35                  40                  45

Asn Ala Leu Ile Thr Thr Asn Ala Thr Cys Gly Glu Lys Gly Pro Glu
     50                  55                  60

Met Tyr Cys Lys Leu Val Glu His Val Pro Gly Gln Pro Val Arg Asn
 65                  70                  75                  80

Pro Gln Cys Arg Ile Cys Asn Gln Asn Ser Ser Asn Pro Asn Gln Arg
                 85                  90                  95

His Pro Ile Thr Asn Ala Ile Asp Gly Lys Asn Thr Trp Trp Gln Ser
            100                 105                 110

Pro Ser Ile Lys Asn Gly Ile Glu Tyr His Tyr Val Thr Ile Thr Leu
        115                 120                 125

Asp Leu Gln Gln Val Phe Gln Ile Ala Tyr Val Ile Val Lys Ala Ala
    130                 135                 140

Asn Ser Pro Arg Pro Gly Asn Trp Ile Leu Glu Arg Ser Leu Asp Asp
145                 150                 155                 160
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Val Glu Tyr Lys Pro Trp Gln Tyr His Ala Val Thr Asp Thr Glu Cys
                165                 170                 175

Leu Thr Leu Tyr Asn Ile Tyr Pro Arg Thr Gly Pro Pro Ser Tyr Ala
            180                 185                 190

Lys Asp Asp Glu Val Ile Cys Thr Ser Phe Tyr Ser Lys Ile His Pro
        195                 200                 205

Leu Glu Asn Gly Glu Ile His Ile Ser Leu Ile Asn Gly Arg Pro Ser
    210                 215                 220

Ala Asp Asp Pro Ser Pro Glu Leu Leu Glu Phe Thr Ser Ala Arg Tyr
225                 230                 235                 240

Ile Arg Leu Arg Phe Gln Arg Ile Arg Thr Leu Asn Ala Asp Leu Met
                245                 250                 255

Met Phe Ala His Lys Asp Pro Arg Glu Ile Asp Pro Ile Val Thr Arg
            260                 265                 270

Arg Tyr Tyr Tyr Ser Val Lys Asp Ile Ser Val Gly Gly Met Cys Ile
        275                 280                 285

Cys Tyr Gly His Ala Arg Ala Cys Pro Leu Asp Pro Ala Thr Asn Lys
    290                 295                 300

Ser Arg Cys Glu Cys Glu His Asn Thr Cys Gly Asp Ser Cys Asp Gln
305                 310                 315                 320

Cys Cys Pro Gly Phe His Gln Lys Pro Trp Arg Ala Gly Thr Phe Leu
                325                 330                 335

Thr Lys Thr Glu Cys Glu Ala Cys Asn Cys His Gly Lys Ala Glu Glu
            340                 345                 350

Cys Tyr Tyr Asp Glu Asn Val Ala Arg Arg Asn Leu Ser Leu Asn Ile
        355                 360                 365

Arg Gly Lys Tyr Ile Gly Gly Gly Val Cys Ile Asn Cys Thr Gln Asn
    370                 375                 380

Thr Ala Gly Ile Asn Cys Glu Thr Cys Thr Asp Gly Phe Phe Arg Pro
385                 390                 395                 400

Lys Gly Val Ser Pro Asn Tyr Pro Arg Pro Cys Gln Pro Cys His Cys
                405                 410                 415

Asp Pro Ile Gly Ser Leu Asn Glu Val Cys Val Lys Asp Glu Lys His
            420                 425                 430

Ala Arg Arg Gly Leu Ala Pro Gly Ser Cys His Cys Lys Thr Gly Phe
        435                 440                 445

Gly Gly Val Ser Cys Asp Arg Cys Ala Arg Gly Tyr Thr Gly Tyr Pro
    450                 455                 460

Asp Cys Lys Ala Cys Asn Cys Ser Gly Leu Gly Ser Lys Asn Glu Asp
465                 470                 475                 480

Pro Cys Phe Gly Pro Cys Ile Cys Lys Glu Asn Val Glu Gly Gly Asp
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                485                 490                 495

Cys Ser Arg Cys Lys Ser Gly Phe Phe Asn Leu Gln Glu Asp Asn Trp
            500                 505                 510

Lys Gly Cys Asp Glu Cys Phe Cys Ser Gly Val Ser Asn Arg Cys Gln
        515                 520                 525

Ser Ser Tyr Trp Thr Tyr Gly Lys Ile Gln Asp Met Ser Gly Trp Tyr
    530                 535                 540

Leu Thr Asp Leu Pro Gly Arg Ile Arg Val Ala Pro Gln Gln Asp Asp
545                 550                 555                 560

Leu Asp Ser Pro Gln Gln Ile Ser Ile Ser Asn Ala Glu Ala Arg Gln
                565                 570                 575

Ala Leu Pro His Ser Tyr Tyr Trp Ser Ala Pro Ala Pro Tyr Leu Gly
            580                 585                 590

Asn Lys Leu Pro Ala Val Gly Gly Gln Leu Thr Phe Thr Ile Ser Tyr
        595                 600                 605

Asp Leu Glu Glu Glu Glu Glu Asp Thr Glu Arg Val Leu Gln Leu Met
    610                 615                 620

Ile Ile Leu Glu Gly Asn Asp Leu Ser Ile Ser Thr Ala Gln Asp Glu
625                 630                 635                 640

Val Tyr Leu His Pro Ser Glu Glu His Thr Asn Val Leu Leu Leu Lys
                645                 650                 655

Glu Glu Ser Phe Thr Ile His Gly Thr His Phe Pro Val Arg Arg Lys
            660                 665                 670

Glu Phe Met Thr Val Leu Ala Asn Leu Lys Arg Val Leu Leu Gln Ile
        675                 680                 685

Thr Tyr Ser Phe Gly Met Asp Ala Ile Phe Arg Leu Ser Ser Val Asn
    690                 695                 700

Leu Glu Ser Ala Val Ser Tyr Pro Thr Asp Gly Ser Ile Ala Ala Ala
705                 710                 715                 720

Val Glu Val Cys Gln Cys Pro Pro Gly Tyr Thr Gly Ser Ser Cys Glu
                725                 730                 735

Ser Cys Trp Pro Arg His Arg Arg Val Asn Gly Thr Ile Phe Gly Gly
            740                 745                 750

Ile Cys Glu Pro Cys Gln Cys Phe Gly His Ala Glu Ser Cys Asp Asp
        755                 760                 765

Val Thr Gly Glu Cys Leu Asn Cys Lys Asp His Thr Gly Gly Pro Tyr
    770                 775                 780

Cys Asp Lys Cys Leu Pro Gly Phe Tyr Gly Glu Pro Thr Lys Gly Thr
785                 790                 795                 800

Ser Glu Asp Cys Gln Pro Cys Ala Cys Pro Leu Asn Ile Pro Ser Asn
                805                 810                 815
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Asn Phe Ser Pro Thr Cys His Leu Asp Arg Ser Leu Gly Leu Ile Cys
            820                 825                 830

Asp Gly Cys Pro Val Gly Tyr Thr Gly Pro Arg Cys Glu Arg Cys Ala
        835                 840                 845

Glu Gly Tyr Phe Gly Gln Pro Ser Val Pro Gly Gly Ser Cys Gln Pro
    850                 855                 860

Cys Gln Cys Asn Asp Asn Leu Asp Phe Ser Ile Pro Gly Ser Cys Asp
865                 870                 875                 880

Ser Leu Ser Gly Ser Cys Leu Ile Cys Lys Pro Gly Thr Thr Gly Arg
                885                 890                 895

Tyr Cys Glu Leu Cys Ala Asp Gly Tyr Phe Gly Asp Ala Val Asp Ala
            900                 905                 910

Lys Asn Cys Gln Pro Cys Arg Cys Asn Ala Gly Gly Ser Phe Ser Glu
        915                 920                 925

Val Cys His Ser Gln Thr Gly Gln Cys Glu Cys Arg Ala Asn Val Gln
    930                 935                 940

Gly Gln Arg Cys Asp Lys Cys Lys Ala Gly Thr Phe Gly Leu Gln Ser
945                 950                 955                 960

Ala Arg Gly Cys Val Pro Cys Asn Cys Asn Ser Phe Gly Ser Lys Ser
                965                 970                 975

Phe Asp Cys Glu Glu Ser Gly Gln Cys Trp Cys Gln Pro Gly Val Thr
            980                 985                 990

Gly Lys Lys Cys Asp Arg Cys Ala His Gly Tyr Phe Asn Phe Gln Glu
        995                1000                1005

Gly Gly Cys Thr Ala Cys Glu Cys Ser His Leu Gly Asn Asn Cys Asp
   1010                1015                1020

Pro Lys Thr Gly Arg Cys Ile Cys Pro Pro Asn Thr Ile Gly Glu Lys
025                1030                1035                1040

Cys Ser Lys Cys Ala Pro Asn Thr Trp Gly His Ser Ile Thr Thr Gly
               1045                1050                1055

Cys Lys Ala Cys Asn Cys Ser Thr Val Gly Ser Leu Asp Phe Gln Cys
           1060                1065                1070

Asn Val Asn Thr Gly Gln Cys Asn Cys His Pro Lys Phe Ser Gly Ala
       1075                1080                1085

Lys Cys Thr Glu Cys Ser Arg Gly His Trp Asn Tyr Pro Arg Cys Asn
   1090                1095                1100

Leu Cys Asp Cys Phe Leu Pro Gly Thr Asp Ala Thr Thr Cys Asp Ser
105                1110                1115                1120

Glu Thr Lys Lys Cys Ser Cys Ser Asp Gln Thr Gly Gln Cys Thr Cys
               1125                1130                1135
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Lys Val Asn Val Glu Gly Ile His Cys Asp Arg Cys Arg Pro Gly Lys
            1140                1145                1150

Phe Gly Leu Asp Ala Lys Asn Pro Leu Gly Cys Ser Ser Cys Tyr Cys
        1155                1160                1165

Phe Gly Thr Thr Thr Gln Cys Ser Glu Ala Lys Gly Leu Ile Arg Thr
    1170                1175                1180

Trp Val Thr Leu Lys Ala Glu Gln Thr Ile Leu Pro Leu Val Asp Glu
185                 1190                1195                1200

Ala Leu Gln His Thr Thr Thr Lys Gly Ile Val Phe Gln His Pro Glu
                1205                1210                1215

Ile Val Ala His Met Asp Leu Met Arg Glu Asp Leu His Leu Glu Pro
            1220                1225                1230

Phe Tyr Trp Lys Leu Pro Glu Gln Phe Glu Gly Lys Lys Leu Met Ala
        1235                1240                1245

Tyr Gly Gly Lys Leu Lys Tyr Ala Ile Tyr Phe Glu Ala Arg Glu Glu
    1250                1255                1260

Thr Gly Phe Ser Thr Tyr Asn Pro Gln Val Ile Ile Arg Gly Gly Thr
265                 1270                1275                1280

Pro Thr His Ala Arg Ile Ile Val Arg His Met Ala Ala Pro Leu Ile
                1285                1290                1295

Gly Gln Leu Thr Arg His Glu Ile Glu Met Thr Glu Lys Glu Trp Lys
            1300                1305                1310

Tyr Tyr Gly Asp Asp Pro Arg Val His Arg Thr Val Thr Arg Glu Asp
        1315                1320                1325

Phe Leu Asp Ile Leu Tyr Asp Ile His Tyr Ile Leu Ile Lys Ala Thr
    1330                1335                1340

Tyr Gly Asn Phe Met Arg Gln Ser Arg Ile Ser Glu Ile Ser Met Glu
345                 1350                1355                1360

Val Ala Glu Gln Gly Arg Gly Thr Thr Met Thr Pro Pro Ala Asp Leu
                1365                1370                1375

Ile Glu Lys Cys Asp Cys Pro Leu Gly Tyr Ser Gly Leu Ser Cys Glu
            1380                1385                1390

Ala Cys Leu Pro Gly Phe Tyr Arg Leu Arg Ser Gln Pro Gly Gly Arg
        1395                1400                1405

Thr Pro Gly Pro Thr Leu Gly Thr Cys Val Pro Cys Gln Cys Asn Gly
    1410                1415                1420

His Ser Ser Leu Cys Asp Pro Glu Thr Ser Ile Cys Gln Asn Cys Gln
425                 1430                1435                1440

His His Thr Ala Gly Asp Phe Cys Glu Arg Cys Ala Leu Gly Tyr Tyr
                1445                1450                1455

Gly Ile Val Lys Gly Leu Pro Asn Asp Cys Gln Gln Cys Ala Cys Pro
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            1460                1465                1470

Leu Ile Ser Ser Ser Asn Asn Phe Ser Pro Ser Cys Val Ala Glu Gly
       1475                1480                1485

Leu Asp Asp Tyr Arg Cys Thr Ala Cys Pro Arg Gly Tyr Glu Gly Gln
   1490                1495                1500

Tyr Cys Glu Arg Cys Ala Pro Gly Tyr Thr Gly Ser Pro Gly Asn Pro
505                1510                1515                1520

Gly Gly Ser Cys Gln Glu Cys Glu Cys Asp Pro Tyr Gly Ser Leu Pro
               1525                1530                1535

Val Pro Cys Asp Pro Val Thr Gly Phe Cys Thr Cys Arg Pro Gly Ala
            1540                1545                1550

Thr Gly Arg Lys Cys Asp Gly Cys Lys His Trp His Ala Arg Glu Gly
       1555                1560                1565

Trp Glu Cys Val Phe Cys Gly Asp Glu Cys Thr Gly Leu Leu Leu Gly
   1570                1575                1580

Asp Leu Ala Arg Leu Glu Gln Met Val Met Ser Ile Asn Leu Thr Gly
585                1590                1595                1600

Pro Leu Pro Ala Pro Tyr Lys Met Leu Tyr Gly Leu Glu Asn Met Thr
               1605                1610                1615

Gln Glu Leu Lys His Leu Leu Ser Pro Gln Arg Ala Pro Glu Arg Leu
            1620                1625                1630

Ile Gln Leu Ala Glu Gly Asn Leu Asn Thr Leu Val Thr Glu Met Asn
       1635                1640                1645

Glu Leu Leu Thr Arg Ala Thr Lys Val Thr Ala Asp Gly Glu Gln Thr
   1650                1655                1660

Gly Gln Asp Ala Glu Arg Thr Asn Thr Arg Ala Lys Ser Leu Gly Glu
665                1670                1675                1680

Phe Ile Lys Glu Leu Ala Arg Asp Ala Glu Ala Val Asn Glu Lys Ala
               1685                1690                1695

Ile Lys Leu Asn Glu Thr Leu Gly Thr Arg Asp Glu Ala Phe Glu Arg
            1700                1705                1710

Asn Leu Glu Gly Leu Gln Lys Glu Ile Asp Gln Met Ile Lys Glu Leu
       1715                1720                1725

Arg Arg Lys Asn Leu Glu Thr Gln Lys Glu Ile Ala Glu Asp Glu Leu
   1730                1735                1740

Val Ala Ala Glu Ala Leu Leu Lys Lys Val Lys Lys Leu Phe Gly Glu
745                1750                1755                1760

Ser Arg Gly Glu Asn Glu Glu Met Glu Lys Asp Leu Arg Glu Lys Leu
               1765                1770                1775

Ala Asp Tyr Lys Asn Lys Val Asp Asp Ala Trp Asp Leu Leu Arg Glu
            1780                1785                1790
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Ala Thr Asp Lys Ile Arg Glu Ala Asn Arg Leu Phe Ala Val Asn Gln
       1795                1800                1805

Lys Asn Met Thr Ala Leu Glu Lys Lys Lys Glu Ala Val Glu Ser Gly
   1810                1815                1820

Lys Arg Gln Ile Glu Asn Thr Leu Lys Glu Gly Asn Asp Ile Leu Asp
825                1830                1835                1840

Glu Ala Asn Arg Leu Ala Asp Glu Ile Asn Ser Ile Ile Asp Tyr Val
               1845                1850                1855

Glu Asp Ile Gln Thr Lys Leu Pro Pro Met Ser Glu Glu Leu Asn Asp
           1860                1865                1870

Lys Ile Asp Asp Leu Ser Gln Glu Ile Lys Asp Arg Lys Leu Ala Glu
       1875                1880                1885

Lys Val Ser Gln Ala Glu Ser His Ala Ala Gln Leu Asn Asp Ser Ser
   1890                1895                1900

Ala Val Leu Asp Gly Ile Leu Asp Glu Ala Lys Asn Ile Ser Phe Asn
905                1910                1915                1920

Ala Thr Ala Ala Phe Lys Ala Tyr Ser Asn Ile Lys Asp Tyr Ile Asp
               1925                1930                1935

Glu Ala Glu Lys Val Ala Lys Glu Ala Lys Asp Leu Ala His Glu Ala
           1940                1945                1950

Thr Lys Leu Ala Thr Gly Pro Arg Gly Leu Leu Lys Glu Asp Ala Lys
       1955                1960                1965

Gly Cys Leu Gln Lys Ser Phe Arg Ile Leu Asn Glu Ala Lys Lys Leu
   1970                1975                1980

Ala Asn Asp Val Lys Glu Asn Glu Asp His Leu Asn Gly Leu Lys Thr
985                1990                1995                2000

Arg Ile Glu Asn Ala Asp Ala Arg Asn Gly Asp Leu Leu Arg Thr Leu
               2005                2010                2015

Asn Asp Thr Leu Gly Lys Leu Ser Ala Ile Pro Asn Asp Thr Ala Ala
           2020                2025                2030

Lys Leu Gln Ala Val Lys Asp Lys Ala Arg Gln Ala Asn Asp Thr Ala
       2035                2040                2045

Lys Asp Val Leu Ala Gln Ile Thr Glu Leu His Gln Asn Leu Asp Gly
   2050                2055                2060

Leu Lys Lys Asn Tyr Asn Lys Leu Ala Asp Ser Val Ala Lys Thr Asn
065                2070                2075                2080

Ala Val Val Lys Asp Pro Ser Lys Asn Lys Ile Ile Ala Asp Ala Asp
               2085                2090                2095

Ala Thr Val Lys Asn Leu Glu Gln Glu Ala Asp Arg Leu Ile Asp Lys
           2100                2105                2110
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Leu Lys Pro Ile Lys Glu Leu Glu Asp Asn Leu Lys Lys Asn Ile Ser
      2115                2120                2125

Glu Ile Lys Glu Leu Ile Asn Gln Ala Arg Lys Gln Ala Asn Ser Ile
   2130                2135                2140

Lys Val Ser Val Ser Ser Gly Gly Asp Cys Ile Arg Thr Tyr Lys Pro
145                2150                2155                2160

Glu Ile Lys Lys Gly Ser Tyr Asn Asn Ile Val Val Asn Val Lys Thr
              2165                2170                2175

Ala Val Ala Asp Asn Leu Leu Phe Tyr Leu Gly Ser Ala Lys Phe Ile
           2180                2185                2190

Asp Phe Leu Ala Ile Glu Met Arg Lys Gly Lys Val Ser Phe Leu Trp
      2195                2200                2205

Asp Val Gly Ser Gly Val Gly Arg Val Glu Tyr Pro Asp Leu Thr Ile
   2210                2215                2220

Asp Asp Ser Tyr Trp Tyr Arg Ile Val Ala Ser Arg Thr Gly Arg Asn
225                2230                2235                2240

Gly Thr Ile Ser Val Arg Ala Leu Asp Gly Pro Lys Ala Ser Ile Val
              2245                2250                2255

Pro Ser Thr His His Ser Thr Ser Pro Pro Gly Tyr Thr Ile Leu Asp
           2260                2265                2270

Val Asp Ala Asn Ala Met Leu Phe Val Gly Gly Leu Thr Gly Lys Leu
      2275                2280                2285

Lys Lys Ala Asp Ala Val Arg Val Ile Thr Phe Thr Gly Cys Met Gly
   2290                2295                2300

Glu Thr Tyr Phe Asp Asn Lys Pro Ile Gly Leu Trp Asn Phe Arg Glu
305                2310                2315                2320

Lys Glu Gly Asp Cys Lys Gly Cys Thr Val Ser Pro Gln Val Glu Asp
              2325                2330                2335

Ser Glu Gly Thr Ile Gln Phe Asp Gly Glu Gly Tyr Ala Leu Val Ser
           2340                2345                2350

Arg Pro Ile Arg Trp Tyr Pro Asn Ile Ser Thr Val Met Phe Lys Phe
      2355                2360                2365

Arg Thr Phe Ser Ser Ser Ala Leu Leu Met Tyr Leu Ala Thr Arg Asp
   2370                2375                2380

Leu Arg Asp Phe Met Ser Val Glu Leu Thr Asp Gly His Ile Lys Val
385                2390                2395                2400

Ser Tyr Asp Leu Gly Ser Gly Met Ala Ser Val Val Ser Asn Gln Asn
              2405                2410                2415

His Asn Asp Gly Lys Trp Lys Ser Phe Thr Leu Ser Arg Ile Gln Lys
           2420                2425                2430

Gln Ala Asn Ile Ser Ile Val Asp Ile Asp Thr Asn Gln Glu Glu Asn
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      2435                2440                2445

Ile Ala Thr Ser Ser Ser Gly Asn Asn Phe Gly Leu Asp Leu Lys Ala
   2450                2455                2460

Asp Asp Lys Ile Tyr Phe Gly Gly Leu Pro Thr Leu Arg Asn Leu Ser
465                 2470                2475                2480

Met Lys Ala Arg Pro Glu Val Asn Leu Lys Lys Tyr Ser Gly Cys Leu
               2485                2490                2495

Lys Asp Ile Glu Ile Ser Arg Thr Pro Tyr Asn Ile Leu Ser Ser Pro
            2500                2505                2510

Asp Tyr Val Gly Val Thr Lys Gly Cys Ser Leu Glu Asn Val Tyr Thr
       2515                2520                2525

Val Ser Phe Pro Lys Pro Gly Phe Val Glu Leu Ser Pro Val Pro Ile
   2530                2535                2540

Asp Val Gly Thr Glu Ile Asn Leu Ser Phe Ser Thr Lys Asn Glu Ser
545                 2550                2555                2560

Gly Ile Ile Leu Leu Gly Ser Gly Gly Thr Pro Ala Pro Pro Arg Arg
               2565                2570                2575

Lys Arg Arg Gln Thr Gly Gln Ala Tyr Tyr Val Ile Leu Leu Asn Arg
            2580                2585                2590

Gly Arg Leu Glu Val His Leu Ser Thr Gly Ala Arg Thr Met Arg Lys
       2595                2600                2605

Ile Val Ile Arg Pro Glu Pro Asn Leu Phe His Asp Gly Arg Glu His
   2610                2615                2620

Ser Val His Val Glu Arg Thr Arg Gly Ile Phe Thr Val Gln Val Asp
625                 2630                2635                2640

Glu Asn Arg Arg Tyr Met Gln Asn Leu Thr Val Glu Gln Pro Ile Glu
               2645                2650                2655

Val Lys Lys Leu Phe Val Gly Gly Ala Pro Pro Glu Phe Gln Pro Ser
            2660                2665                2670

Pro Leu Arg Asn Ile Pro Pro Phe Glu Gly Cys Ile Trp Asn Leu Val
       2675                2680                2685

Ile Asn Ser Val Pro Met Asp Phe Ala Arg Pro Val Ser Phe Lys Asn
   2690                2695                2700

Ala Asp Ile Gly Arg Cys Ala His Gln Lys Leu Arg Glu Asp Glu Asp
705                 2710                2715                2720

Gly Ala Ala Pro Ala Glu Ile Val Ile Gln Pro Glu Pro Val Pro Thr
               2725                2730                2735

Pro Ala Phe Pro Thr Pro Thr Pro Val Leu Thr His Gly Pro Cys Ala
            2740                2745                2750

Ala Glu Ser Glu Pro Ala Leu Leu Ile Gly Ser Lys Gln Phe Gly Leu
       2755                2760                2765
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Ser Arg Asn Ser His Ile Ala Ile Ala Phe Asp Asp Thr Lys Val Lys
   2770                2775                2780

Asn Arg Leu Thr Ile Glu Leu Glu Val Arg Thr Glu Ala Glu Ser Gly
785                 2790                2795                2800

Leu Leu Phe Tyr Met Ala Ala Ile Asn His Ala Asp Phe Ala Thr Val
               2805                2810                2815

Gln Leu Arg Asn Gly Leu Pro Tyr Phe Ser Tyr Asp Leu Gly Ser Gly
            2820                2825                2830

Asp Thr His Thr Met Ile Pro Thr Lys Ile Asn Asp Gly Gln Trp His
       2835                2840                2845

Lys Ile Lys Ile Met Arg Ser Lys Gln Glu Gly Ile Leu Tyr Val Asp
   2850                2855                2860

Gly Ala Ser Asn Arg Thr Ile Ser Pro Lys Lys Ala Asp Ile Leu Asp
865                 2870                2875                2880

Val Val Gly Met Leu Tyr Val Gly Gly Leu Pro Ile Asn Tyr Thr Thr
               2885                2890                2895

Arg Arg Ile Gly Pro Val Thr Tyr Ser Ile Asp Gly Cys Val Arg Asn
            2900                2905                2910

Leu His Met Ala Glu Ala Pro Ala Asp Leu Glu Gln Pro Thr Ser Ser
       2915                2920                2925

Phe His Val Gly Thr Cys Phe Ala Asn Ala Gln Arg Gly Thr Tyr Phe
   2930                2935                2940

Asp Gly Thr Gly Phe Ala Lys Ala Val Gly Gly Phe Lys Val Gly Leu
945                 2950                2955                2960

Asp Leu Leu Val Glu Phe Glu Phe Ala Thr Thr Thr Thr Thr Gly Val
               2965                2970                2975

Leu Leu Gly Ile Ser Ser Gln Lys Met Asp Gly Met Gly Ile Glu Met
            2980                2985                2990

Ile Asp Glu Lys Leu Met Phe His Val Asp Asn Gly Ala Gly Arg Phe
       2995                3000                3005

Thr Ala Val Tyr Asp Ala Gly Val Pro Gly His Leu Cys Asp Gly Gln
   3010                3015                3020

Trp His Lys Val Thr Ala Asn Lys Ile Lys His Arg Ile Glu Leu Thr
025                 3030                3035                3040

Val Asp Gly Asn Gln Val Glu Ala Gln Ser Pro Asn Pro Ala Ser Thr
               3045                3050                3055

Ser Ala Asp Thr Asn Asp Pro Val Phe Val Gly Gly Phe Pro Asp Asp
            3060                3065                3070

Leu Lys Gln Phe Gly Leu Thr Thr Ser Ile Pro Phe Arg Gly Cys Ile
       3075                3080                3085
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Phe Ala Lys Ala Leu Glu
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Gln Arg Pro Gln Gln Gln Arg Gln Ser Gln Ala His Gln Gln Arg Gly
  1               5                  10                  15

tta ttc cct gct gtc ctg aat ctt gct tct aat gct ctt atc acg acc   96
Leu Phe Pro Ala Val Leu Asn Leu Ala Ser Asn Ala Leu Ile Thr Thr
            20                  25                  30

aat gca aca tgt gga gaa aaa gga cct gaa atg tac tgc aaa ttg gta   144
Asn Ala Thr Cys Gly Glu Lys Gly Pro Glu Met Tyr Cys Lys Leu Val
        35                  40                  45

gaa cat gtc cct ggg cag cct gtg agg aac ccg cag tgt cga atc tgc   192
Glu His Val Pro Gly Gln Pro Val Arg Asn Pro Gln Cys Arg Ile Cys
    50                  55                  60

aat caa aac agc agc aat cca aac cag aga cac ccg att aca aat gct   240
Asn Gln Asn Ser Ser Asn Pro Asn Gln Arg His Pro Ile Thr Asn Ala
65                  70                  75                  80

att gat gga aag aac act tgg tgg cag agt ccc agt att aag aat gga   288
Ile Asp Gly Lys Asn Thr Trp Trp Gln Ser Pro Ser Ile Lys Asn Gly
                85                  90                  95

atc gaa tac cat tat gtg aca att aca ctg gat tta cag cag gtg ttc   336
Ile Glu Tyr His Tyr Val Thr Ile Thr Leu Asp Leu Gln Gln Val Phe
            100                 105                 110

cag atc gcg tat gtg att gtg aag gca gct aac tcc ccc cgg cct gga   384
Gln Ile Ala Tyr Val Ile Val Lys Ala Ala Asn Ser Pro Arg Pro Gly
        115                 120                 125

aac tgg att ttg gaa cgc tct ctt gat gat gtt gaa tac aag ccc tgg   432
Asn Trp Ile Leu Glu Arg Ser Leu Asp Asp Val Glu Tyr Lys Pro Trp
    130                 135                 140

cag tat cat gct gtg aca gac acg gag tgc cta acg ctt tac aat att   480
Gln Tyr His Ala Val Thr Asp Thr Glu Cys Leu Thr Leu Tyr Asn Ile
145                 150                 155                 160

tat ccc cgc act ggg cca ccg tca tat gcc aaa gat gat gag gtc atc   528
Tyr Pro Arg Thr Gly Pro Pro Ser Tyr Ala Lys Asp Asp Glu Val Ile
                165                 170                 175
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tgc act tca ttt tac tcc aag ata cac ccc tta gaa aat gga gag att   576
Cys Thr Ser Phe Tyr Ser Lys Ile His Pro Leu Glu Asn Gly Glu Ile
            180                 185                 190

cac atc tct tta atc aat ggg aga cca agt gcc gat gat cct tct cca   624
His Ile Ser Leu Ile Asn Gly Arg Pro Ser Ala Asp Asp Pro Ser Pro
        195                 200                 205

gaa ctg cta gaa ttt acc tcc gct cgc tat att cgc ctg aga ttt cag   672
Glu Leu Leu Glu Phe Thr Ser Ala Arg Tyr Ile Arg Leu Arg Phe Gln
    210                 215                 220

agg atc cgc aca ctg aat gct gac ttg atg atg ttt gct cac aaa gac   720
Arg Ile Arg Thr Leu Asn Ala Asp Leu Met Met Phe Ala His Lys Asp
225                 230                 235                 240

cca aga gaa att gac ccc att gtc acc aga aga tat tac tac tcg gtc   768
Pro Arg Glu Ile Asp Pro Ile Val Thr Arg Arg Tyr Tyr Tyr Ser Val
                245                 250                 255

aag gat att tca gtt gga ggg atg tgc atc tgc tat ggt cat gcc agg   816
Lys Asp Ile Ser Val Gly Gly Met Cys Ile Cys Tyr Gly His Ala Arg
            260                 265                 270

gct tgt cca ctt gat cca gcg aca aat aaa tct cgc tgt gag tgt gag   864
Ala Cys Pro Leu Asp Pro Ala Thr Asn Lys Ser Arg Cys Glu Cys Glu
        275                 280                 285

cat aac aca tgt ggc gat agc tgt gat cag tgc tgt cca gga ttc cat   912
His Asn Thr Cys Gly Asp Ser Cys Asp Gln Cys Cys Pro Gly Phe His
    290                 295                 300

cag aaa ccc tgg aga gct gga act ttt cta act aaa act gaa tgt gaa   960
Gln Lys Pro Trp Arg Ala Gly Thr Phe Leu Thr Lys Thr Glu Cys Glu
305                 310                 315                 320

gca tgc aat tgt cat gga aaa gct gaa gaa tgc tat tat gat gaa aat  1008
Ala Cys Asn Cys His Gly Lys Ala Glu Glu Cys Tyr Tyr Asp Glu Asn
                325                 330                 335

gtt gcc aga aga aat ctg agt ttg aat ata cgt gga aag tac att gga  1056
Val Ala Arg Arg Asn Leu Ser Leu Asn Ile Arg Gly Lys Tyr Ile Gly
            340                 345                 350

ggg ggt gtc tgc att aat tgt acc caa aac act gct ggt ata aac tgc  1104
Gly Gly Val Cys Ile Asn Cys Thr Gln Asn Thr Ala Gly Ile Asn Cys
        355                 360                 365

gag aca tgt aca gat ggc ttc ttc aga ccc aaa ggg gta tct cca aat  1152
Glu Thr Cys Thr Asp Gly Phe Phe Arg Pro Lys Gly Val Ser Pro Asn
    370                 375                 380

tat cca agg cca tgc cag cca tgt cat tgc gat cca att ggt tcc tta  1200
Tyr Pro Arg Pro Cys Gln Pro Cys His Cys Asp Pro Ile Gly Ser Leu
385                 390                 395                 400

aat gaa gtc tgt gtc aag gat gag aaa cat gct cga cga ggt ttg gca  1248
Asn Glu Val Cys Val Lys Asp Glu Lys His Ala Arg Arg Gly Leu Ala
                405                 410                 415

cct gga tcc tgt cat tgc aaa act ggt ttt gga ggt gtg agc tgt gat  1296
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Pro Gly Ser Cys His Cys Lys Thr Gly Phe Gly Gly Val Ser Cys Asp
            420                 425                 430

cgg tgt gcc agg ggc tac act ggc tac ccg gac tgc aaa gcc tgt aac   1344
Arg Cys Ala Arg Gly Tyr Thr Gly Tyr Pro Asp Cys Lys Ala Cys Asn
        435                 440                 445

tgc agt ggg tta ggg agc aaa aat gag gat cct tgt ttt ggc ccc tgt   1392
Cys Ser Gly Leu Gly Ser Lys Asn Glu Asp Pro Cys Phe Gly Pro Cys
    450                 455                 460

atc tgc aag gaa aat gtt gaa gga gga gac tgt agt cgt tgc aaa tcc   1440
Ile Cys Lys Glu Asn Val Glu Gly Gly Asp Cys Ser Arg Cys Lys Ser
465                 470                 475                 480

ggc ttc ttc aat ttg caa gag gat aat tgg aaa ggc tgc gat gag tgt   1488
Gly Phe Phe Asn Leu Gln Glu Asp Asn Trp Lys Gly Cys Asp Glu Cys
                485                 490                 495

ttc tgt tca ggg gtt tca aac aga tgt cag agt tcc tac tgg acc tat   1536
Phe Cys Ser Gly Val Ser Asn Arg Cys Gln Ser Ser Tyr Trp Thr Tyr
            500                 505                 510

ggc aaa ata caa gat atg agt ggc tgg tat ctg act gac ctt cct ggc   1584
Gly Lys Ile Gln Asp Met Ser Gly Trp Tyr Leu Thr Asp Leu Pro Gly
        515                 520                 525

cgc att cga gtg gct ccc cag cag gac gac ttg gac tca cct cag cag   1632
Arg Ile Arg Val Ala Pro Gln Gln Asp Asp Leu Asp Ser Pro Gln Gln
    530                 535                 540

atc agc atc agt aac gcg gag gcc cgg caa gcc ctg ccg cac agc tac   1680
Ile Ser Ile Ser Asn Ala Glu Ala Arg Gln Ala Leu Pro His Ser Tyr
545                 550                 555                 560

tac tgg agc gcg ccg gct ccc tat ctg gga aac aaa ctc cca gca gta   1728
Tyr Trp Ser Ala Pro Ala Pro Tyr Leu Gly Asn Lys Leu Pro Ala Val
                565                 570                 575

gga gga cag ttg aca ttt acc ata tca tat gac ctt gaa gaa gag gaa   1776
Gly Gly Gln Leu Thr Phe Thr Ile Ser Tyr Asp Leu Glu Glu Glu Glu
            580                 585                 590

gaa gat aca gaa cgt gtt ctc cag ctt atg att atc tta gag ggt aat   1824
Glu Asp Thr Glu Arg Val Leu Gln Leu Met Ile Ile Leu Glu Gly Asn
        595                 600                 605

gac ttg agc atc agc aca gcc caa gat gag gtg tac ctg cac cca tct   1872
Asp Leu Ser Ile Ser Thr Ala Gln Asp Glu Val Tyr Leu His Pro Ser
    610                 615                 620

gaa gaa cat act aat gta ttg tta ctt aaa gaa gaa tca ttt acc ata   1920
Glu Glu His Thr Asn Val Leu Leu Leu Lys Glu Glu Ser Phe Thr Ile
625                 630                 635                 640

cat ggc aca cat ttt cca gtc cgt aga aag gaa ttt atg aca gtg ctt   1968
His Gly Thr His Phe Pro Val Arg Arg Lys Glu Phe Met Thr Val Leu
                645                 650                 655

gcg aat ttg aag aga gtc ctc cta caa atc aca tac agc ttt ggg atg   2016
Ala Asn Leu Lys Arg Val Leu Leu Gln Ile Thr Tyr Ser Phe Gly Met
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            660                 665                 670

gat gcc atc ttc agg ttg agc tct gtt aac ctt gaa tcc gct gtc tcc   2064
Asp Ala Ile Phe Arg Leu Ser Ser Val Asn Leu Glu Ser Ala Val Ser
        675                 680                 685

tat cct act gat gga agc att gca gca gct gta gaa gtg tgt cag tgc   2112
Tyr Pro Thr Asp Gly Ser Ile Ala Ala Ala Val Glu Val Cys Gln Cys
    690                 695                 700

cca cca ggg tat act ggc tcc tct tgt gaa tct tgt tgg cct agg cac   2160
Pro Pro Gly Tyr Thr Gly Ser Ser Cys Glu Ser Cys Trp Pro Arg His
705                 710                 715                 720

agg cga gtt aac ggc act att ttt ggt ggc atc tgt gag cca tgt cag   2208
Arg Arg Val Asn Gly Thr Ile Phe Gly Gly Ile Cys Glu Pro Cys Gln
                725                 730                 735

tgc ttt ggt cat gcg gag tcc tgt gat gac gtc act gga gaa tgc ctg   2256
Cys Phe Gly His Ala Glu Ser Cys Asp Asp Val Thr Gly Glu Cys Leu
            740                 745                 750

aac tgt aag gat cac aca ggt ggc cca tat tgt gat aaa tgt ctt cct   2304
Asn Cys Lys Asp His Thr Gly Gly Pro Tyr Cys Asp Lys Cys Leu Pro
        755                 760                 765

ggt ttc tat ggc gag cct act aaa gga acc tct gaa gac tgt caa ccc   2352
Gly Phe Tyr Gly Glu Pro Thr Lys Gly Thr Ser Glu Asp Cys Gln Pro
    770                 775                 780

tgt gcc tgt cca ctc aat atc cca tcc aat aac ttt agc cca acg tgc   2400
Cys Ala Cys Pro Leu Asn Ile Pro Ser Asn Asn Phe Ser Pro Thr Cys
785                 790                 795                 800

cat tta gac cgg agt ctt gga ttg atc tgt gat gga tgc cct gtc ggg   2448
His Leu Asp Arg Ser Leu Gly Leu Ile Cys Asp Gly Cys Pro Val Gly
                805                 810                 815

tac aca gga cca cgc tgt gag agg tgt gca gaa ggc tat ttt gga caa   2496
Tyr Thr Gly Pro Arg Cys Glu Arg Cys Ala Glu Gly Tyr Phe Gly Gln
            820                 825                 830

ccc tct gta cct gga gga tca tgt cag cca tgc caa tgc aat gac aac   2544
Pro Ser Val Pro Gly Gly Ser Cys Gln Pro Cys Gln Cys Asn Asp Asn
        835                 840                 845

ctt gac ttc tcc atc cct ggc agc tgt gac agc ttg tct ggc tcc tgt   2592
Leu Asp Phe Ser Ile Pro Gly Ser Cys Asp Ser Leu Ser Gly Ser Cys
    850                 855                 860

ctg ata tgt aaa cca ggt aca aca ggc cgg tac tgt gag ctc tgt gct   2640
Leu Ile Cys Lys Pro Gly Thr Thr Gly Arg Tyr Cys Glu Leu Cys Ala
865                 870                 875                 880

gat gga tat ttt gga gat gca gtt gat gcg aag aac tgt cag ccc tgt   2688
Asp Gly Tyr Phe Gly Asp Ala Val Asp Ala Lys Asn Cys Gln Pro Cys
                885                 890                 895

cgc tgt aat gcc ggt ggc tct ttc tct gag gtt tgc cac agt caa act   2736
Arg Cys Asn Ala Gly Gly Ser Phe Ser Glu Val Cys His Ser Gln Thr
            900                 905                 910
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gga cag tgt gag tgc aga gcc aac gtt cag ggt cag aga tgt gac aaa   2784
Gly Gln Cys Glu Cys Arg Ala Asn Val Gln Gly Gln Arg Cys Asp Lys
        915                 920                 925

tgc aag gct ggg acc ttt ggc cta caa tca gca agg ggc tgt gtt ccc   2832
Cys Lys Ala Gly Thr Phe Gly Leu Gln Ser Ala Arg Gly Cys Val Pro
    930                 935                 940

tgc aac tgc aat tct ttt ggg tct aag tca ttc gac tgt gaa gag agt   2880
Cys Asn Cys Asn Ser Phe Gly Ser Lys Ser Phe Asp Cys Glu Glu Ser
945                 950                 955                 960

gga caa tgt tgg tgc caa cct gga gtc aca ggg aag aaa tgt gac cgc   2928
Gly Gln Cys Trp Cys Gln Pro Gly Val Thr Gly Lys Lys Cys Asp Arg
                965                 970                 975

tgt gcc cac ggc tat ttc aac ttc caa gaa gga ggc tgc aca gct tgt   2976
Cys Ala His Gly Tyr Phe Asn Phe Gln Glu Gly Gly Cys Thr Ala Cys
            980                 985                 990

gaa tgt tct cat ctg ggt aat aat tgt gac cca aag act ggg cga tgc   3024
Glu Cys Ser His Leu Gly Asn Asn Cys Asp Pro Lys Thr Gly Arg Cys
        995                1000                1005

att tgc cca ccc aat acc att gga gag aaa tgt tct aaa tgt gca ccc   3072
Ile Cys Pro Pro Asn Thr Ile Gly Glu Lys Cys Ser Lys Cys Ala Pro
   1010                1015                1020

aat acc tgg ggc cac agc att acc act ggt tgt aag gct tgt aac tgc   3120
Asn Thr Trp Gly His Ser Ile Thr Thr Gly Cys Lys Ala Cys Asn Cys
1025                1030                1035                1040

agc aca gtg gga tcc ttg gat ttc caa tgc aat gta aat aca ggc caa   3168
Ser Thr Val Gly Ser Leu Asp Phe Gln Cys Asn Val Asn Thr Gly Gln
                1045                1050                1055

tgc aac tgt cat cca aaa ttc tct ggt gca aaa tgt aca gag tgc agt   3216
Cys Asn Cys His Pro Lys Phe Ser Gly Ala Lys Cys Thr Glu Cys Ser
            1060                1065                1070

cga ggt cac tgg aac tac cct cgc tgc aat ctc tgt gac tgc ttc ctc   3264
Arg Gly His Trp Asn Tyr Pro Arg Cys Asn Leu Cys Asp Cys Phe Leu
        1075                1080                1085

cct ggg aca gat gcc aca acc tgt gat tca gag act aaa aaa tgc tcc   3312
Pro Gly Thr Asp Ala Thr Thr Cys Asp Ser Glu Thr Lys Lys Cys Ser
   1090                1095                1100

tgt agt gat caa act ggg cag tgc act tgt aag gtg aat gtg gaa ggc   3360
Cys Ser Asp Gln Thr Gly Gln Cys Thr Cys Lys Val Asn Val Glu Gly
1105                1110                1115                1120

atc cac tgt gac aga tgc cgg cct ggc aaa ttc gga ctc gat gcc aag   3408
Ile His Cys Asp Arg Cys Arg Pro Gly Lys Phe Gly Leu Asp Ala Lys
                1125                1130                1135

aat cca ctt ggc tgc agc agc tgc tat tgc ttc ggc act act acc cag   3456
Asn Pro Leu Gly Cys Ser Ser Cys Tyr Cys Phe Gly Thr Thr Thr Gln
            1140                1145                1150
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tgc tct gaa gca aaa gga ctg atc cgg acg tgg gtg act ctg aag gct   3504
Cys Ser Glu Ala Lys Gly Leu Ile Arg Thr Trp Val Thr Leu Lys Ala
       1155                1160                1165

gag cag acc att cta ccc ctg gta gat gag gct ctg cag cac acg acc   3552
Glu Gln Thr Ile Leu Pro Leu Val Asp Glu Ala Leu Gln His Thr Thr
   1170                1175                1180

acc aag ggc att gtt ttt caa cat cca gag att gtt gcc cac atg gac   3600
Thr Lys Gly Ile Val Phe Gln His Pro Glu Ile Val Ala His Met Asp
1185                1190                1195                1200

ctg atg aga gaa gat ctc cat ttg gaa cct ttt tat tgg aaa ctt cca   3648
Leu Met Arg Glu Asp Leu His Leu Glu Pro Phe Tyr Trp Lys Leu Pro
               1205                1210                1215

gaa caa ttt gaa gga aag aag ttg atg gcc tat ggg ggc aaa ctc aag   3696
Glu Gln Phe Glu Gly Lys Lys Leu Met Ala Tyr Gly Gly Lys Leu Lys
          1220                1225                1230

tat gca atc tat ttc gag gct cgg gaa gaa aca ggt ttc tct aca tat   3744
Tyr Ala Ile Tyr Phe Glu Ala Arg Glu Glu Thr Gly Phe Ser Thr Tyr
       1235                1240                1245

aat cct caa gtg atc att cga ggt ggg aca cct act cat gct aga att   3792
Asn Pro Gln Val Ile Ile Arg Gly Gly Thr Pro Thr His Ala Arg Ile
   1250                1255                1260

atc gtc agg cat atg gct gct cct ctg att ggc caa ttg aca agg cat   3840
Ile Val Arg His Met Ala Ala Pro Leu Ile Gly Gln Leu Thr Arg His
1265                1270                1275                1280

gaa att gaa atg aca gag aaa gaa tgg aaa tat tat ggg gat gat cct   3888
Glu Ile Glu Met Thr Glu Lys Glu Trp Lys Tyr Tyr Gly Asp Asp Pro
               1285                1290                1295

cga gtc cat aga act gtg acc cga gaa gac ttc ttg gat ata cta tat   3936
Arg Val His Arg Thr Val Thr Arg Glu Asp Phe Leu Asp Ile Leu Tyr
          1300                1305                1310

gat att cat tac att ctt atc aaa gct act tat gga aat ttc atg cga   3984
Asp Ile His Tyr Ile Leu Ile Lys Ala Thr Tyr Gly Asn Phe Met Arg
       1315                1320                1325

caa agc agg att tct gaa atc tca atg gag gta gct gaa caa gga cgt   4032
Gln Ser Arg Ile Ser Glu Ile Ser Met Glu Val Ala Glu Gln Gly Arg
   1330                1335                1340

gga aca aca atg act cct cca gct gac ttg att gaa aaa tgt gat tgt   4080
Gly Thr Thr Met Thr Pro Pro Ala Asp Leu Ile Glu Lys Cys Asp Cys
1345                1350                1355                1360

ccc ctg ggc tat tct ggc ctg tcc tgt gag gca tgc ttg ccg gga ttt   4128
Pro Leu Gly Tyr Ser Gly Leu Ser Cys Glu Ala Cys Leu Pro Gly Phe
               1365                1370                1375

tat cga ctg cgt tct caa cca ggt ggc cgc acc cct gga cca acc ctg   4176
Tyr Arg Leu Arg Ser Gln Pro Gly Gly Arg Thr Pro Gly Pro Thr Leu
          1380                1385                1390

ggc acc tgt gtt cca tgt caa tgt aat gga cac agc agc ctg tgt gac   4224
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Gly Thr Cys Val Pro Cys Gln Cys Asn Gly His Ser Ser Leu Cys Asp
       1395                1400                1405

cct gaa aca tcg ata tgc cag aat tgt caa cat cac act gct ggt gac   4272
Pro Glu Thr Ser Ile Cys Gln Asn Cys Gln His His Thr Ala Gly Asp
   1410                1415                1420

ttc tgt gaa cga tgt gct ctt gga tac tat gga att gtc aag gga ttg   4320
Phe Cys Glu Arg Cys Ala Leu Gly Tyr Tyr Gly Ile Val Lys Gly Leu
1425                1430                1435                1440

cca aat gac tgt cag caa tgt gcc tgc cct ctg att tct tcc agt aac   4368
Pro Asn Asp Cys Gln Gln Cys Ala Cys Pro Leu Ile Ser Ser Ser Asn
               1445                1450                1455

aat ttc agc ccc tct tgt gtc gca gaa gga ctt gac gac tac cgc tgc   4416
Asn Phe Ser Pro Ser Cys Val Ala Glu Gly Leu Asp Asp Tyr Arg Cys
           1460                1465                1470

acg gct tgt cca cgg gga tat gaa ggc cag tac tgt gaa agg tgt gcc   4464
Thr Ala Cys Pro Arg Gly Tyr Glu Gly Gln Tyr Cys Glu Arg Cys Ala
       1475                1480                1485

cct ggc tat act ggc agt cca ggc aac cct gga ggc tcc tgc caa gaa   4512
Pro Gly Tyr Thr Gly Ser Pro Gly Asn Pro Gly Gly Ser Cys Gln Glu
   1490                1495                1500

tgt gag tgt gat ccc tat ggc tca ctg cct gtg ccc tgt gac cct gtc   4560
Cys Glu Cys Asp Pro Tyr Gly Ser Leu Pro Val Pro Cys Asp Pro Val
1505                1510                1515                1520

aca gga ttc tgc acg tgc cga cct gga gcc acg gga agg aag tgt gac   4608
Thr Gly Phe Cys Thr Cys Arg Pro Gly Ala Thr Gly Arg Lys Cys Asp
               1525                1530                1535

ggc tgc aag cac tgg cat gca cgc gag ggc tgg gag tgt gtt ttt tgt   4656
Gly Cys Lys His Trp His Ala Arg Glu Gly Trp Glu Cys Val Phe Cys
           1540                1545                1550

gga gat gag tgc act ggc ctt ctt ctc ggt gac ttg gct cgc ctg gag   4704
Gly Asp Glu Cys Thr Gly Leu Leu Leu Gly Asp Leu Ala Arg Leu Glu
       1555                1560                1565

cag atg gtc atg agc atc aac ctc act ggt ccg ctg cct gcg cca tat   4752
Gln Met Val Met Ser Ile Asn Leu Thr Gly Pro Leu Pro Ala Pro Tyr
   1570                1575                1580

aaa atg ctg tat ggt ctt gaa aat atg act cag gag cta aag cac ttg   4800
Lys Met Leu Tyr Gly Leu Glu Asn Met Thr Gln Glu Leu Lys His Leu
1585                1590                1595                1600

ctg tca cct cag cgg gcc cca gag agg ctt att cag ctg gca gag ggc   4848
Leu Ser Pro Gln Arg Ala Pro Glu Arg Leu Ile Gln Leu Ala Glu Gly
               1605                1610                1615

aat ctg aat aca ctc gtg acc gaa atg aac gag ctg ctg acc agg gct   4896
Asn Leu Asn Thr Leu Val Thr Glu Met Asn Glu Leu Leu Thr Arg Ala
           1620                1625                1630

acc aaa gtg aca gca gat ggc gag cag acc gga cag gat gct gag agg   4944
Thr Lys Val Thr Ala Asp Gly Glu Gln Thr Gly Gln Asp Ala Glu Arg
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      1635                1640                1645

acc aac aca aga gca aag tcc ctg gga gaa ttc att aag gag ctt gcc   4992
Thr Asn Thr Arg Ala Lys Ser Leu Gly Glu Phe Ile Lys Glu Leu Ala
   1650                1655                1660

cgg gat gca gaa gct gta aat gaa aaa gct ata aaa cta aat gaa act   5040
Arg Asp Ala Glu Ala Val Asn Glu Lys Ala Ile Lys Leu Asn Glu Thr
1665                1670                1675                1680

cta gga act cga gac gag gcc ttt gag aga aat ttg gaa ggg ctt cag   5088
Leu Gly Thr Arg Asp Glu Ala Phe Glu Arg Asn Leu Glu Gly Leu Gln
               1685                1690                1695

aaa gag att gac cag atg att aaa gaa ctg agg agg aaa aat cta gag   5136
Lys Glu Ile Asp Gln Met Ile Lys Glu Leu Arg Arg Lys Asn Leu Glu
          1700                1705                1710

aca caa aag gaa att gct gaa gat gag ttg gta gct gca gaa gcc ctt   5184
Thr Gln Lys Glu Ile Ala Glu Asp Glu Leu Val Ala Ala Glu Ala Leu
      1715                1720                1725

ctg aaa aaa gtg aag aag ctg ttt gga gag tcc cgg ggg gaa aat gaa   5232
Leu Lys Lys Val Lys Lys Leu Phe Gly Glu Ser Arg Gly Glu Asn Glu
   1730                1735                1740

gaa atg gag aag gat ctc cgg gaa aaa ctg gct gac tac aaa aac aaa   5280
Glu Met Glu Lys Asp Leu Arg Glu Lys Leu Ala Asp Tyr Lys Asn Lys
1745                1750                1755                1760

gtt gat gat gct tgg gac ctt ttg aga gaa gcc aca gat aaa atc aga   5328
Val Asp Asp Ala Trp Asp Leu Leu Arg Glu Ala Thr Asp Lys Ile Arg
               1765                1770                1775

gaa gct aat cgc cta ttt gca gta aat cag aaa aac atg act gca ttg   5376
Glu Ala Asn Arg Leu Phe Ala Val Asn Gln Lys Asn Met Thr Ala Leu
          1780                1785                1790

gag aaa aag aag gag gct gtt gag agc ggc aaa cga caa att gag aac   5424
Glu Lys Lys Lys Glu Ala Val Glu Ser Gly Lys Arg Gln Ile Glu Asn
      1795                1800                1805

act tta aaa gaa ggc aat gac ata ctc gat gaa gcc aac cgt ctt gca   5472
Thr Leu Lys Glu Gly Asn Asp Ile Leu Asp Glu Ala Asn Arg Leu Ala
   1810                1815                1820

gat gaa atc aac tcc atc ata gac tat gtt gaa gac atc caa act aaa   5520
Asp Glu Ile Asn Ser Ile Ile Asp Tyr Val Glu Asp Ile Gln Thr Lys
1825                1830                1835                1840

ttg cca cct atg tct gag gag ctt aat gat aaa ata gat gac ctc tcc   5568
Leu Pro Pro Met Ser Glu Glu Leu Asn Asp Lys Ile Asp Asp Leu Ser
               1845                1850                1855

caa gaa ata aag gac agg aag ctt gct gag aag gtg tcc cag gct gag   5616
Gln Glu Ile Lys Asp Arg Lys Leu Ala Glu Lys Val Ser Gln Ala Glu
          1860                1865                1870

agc cac gca gct cag ttg aat gac tca tct gct gtc ctt gat gga atc   5664
Ser His Ala Ala Gln Leu Asn Asp Ser Ser Ala Val Leu Asp Gly Ile
      1875                1880                1885
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ctt gat gag gct aaa aac atc tcc ttc aat gcc act gca gcc ttc aaa   5712
Leu Asp Glu Ala Lys Asn Ile Ser Phe Asn Ala Thr Ala Ala Phe Lys
   1890                1895                1900

gct tac agc aat att aag gac tat att gat gaa gct gag aaa gtt gcc   5760
Ala Tyr Ser Asn Ile Lys Asp Tyr Ile Asp Glu Ala Glu Lys Val Ala
1905                1910                1915                1920

aaa gaa gcc aaa gat ctt gca cat gaa gct aca aaa ctg gca aca ggt   5808
Lys Glu Ala Lys Asp Leu Ala His Glu Ala Thr Lys Leu Ala Thr Gly
                1925                1930                1935

cct cgg ggt tta tta aag gaa gat gcc aaa ggc tgt ctt cag aaa agc   5856
Pro Arg Gly Leu Leu Lys Glu Asp Ala Lys Gly Cys Leu Gln Lys Ser
            1940                1945                1950

ttc agg att ctt aac gaa gcc aag aag tta gca aat gat gta aaa gaa   5904
Phe Arg Ile Leu Asn Glu Ala Lys Lys Leu Ala Asn Asp Val Lys Glu
        1955                1960                1965

aat gaa gac cat cta aat ggc tta aaa acc agg ata gaa aat gct gat   5952
Asn Glu Asp His Leu Asn Gly Leu Lys Thr Arg Ile Glu Asn Ala Asp
    1970                1975                1980

gct aga aat ggg gat ctc ttg aga act ttg aat gac act ttg gga aag   6000
Ala Arg Asn Gly Asp Leu Leu Arg Thr Leu Asn Asp Thr Leu Gly Lys
1985                1990                1995                2000

tta tca gct att cca aat gat aca gct gct aaa ctg caa gct gtt aag   6048
Leu Ser Ala Ile Pro Asn Asp Thr Ala Ala Lys Leu Gln Ala Val Lys
                2005                2010                2015

gac aaa gcc aga caa gcc aac gac aca gct aaa gat gta ctg gca cag   6096
Asp Lys Ala Arg Gln Ala Asn Asp Thr Ala Lys Asp Val Leu Ala Gln
            2020                2025                2030

att aca gag ctc cac cag aac ctc gat ggc ctg aag aag aat tac aat   6144
Ile Thr Glu Leu His Gln Asn Leu Asp Gly Leu Lys Lys Asn Tyr Asn
        2035                2040                2045

aaa cta gca gac agc gtc gcc aaa acg aat gct gtg gtt aaa gat cct   6192
Lys Leu Ala Asp Ser Val Ala Lys Thr Asn Ala Val Val Lys Asp Pro
    2050                2055                2060

tcc aag aac aaa atc att gcc gat gca gat gcc act gtc aaa aat tta   6240
Ser Lys Asn Lys Ile Ile Ala Asp Ala Asp Ala Thr Val Lys Asn Leu
2065                2070                2075                2080

gaa cag gaa gct gac cgg cta ata gat aaa ctc aaa ccc atc aag gaa   6288
Glu Gln Glu Ala Asp Arg Leu Ile Asp Lys Leu Lys Pro Ile Lys Glu
                2085                2090                2095

ctt gag gat aac cta aag aaa aac atc tct gag ata aag gaa ttg ata   6336
Leu Glu Asp Asn Leu Lys Lys Asn Ile Ser Glu Ile Lys Glu Leu Ile
            2100                2105                2110

aac caa gct cgg aaa caa gcc aat tct atc aaa gta tct gtg tct tca   6384
Asn Gln Ala Arg Lys Gln Ala Asn Ser Ile Lys Val Ser Val Ser Ser
        2115                2120                2125
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gga ggt gac tgc att cga aca tac aaa cca gaa atc aag aaa gga agt   6432
Gly Gly Asp Cys Ile Arg Thr Tyr Lys Pro Glu Ile Lys Lys Gly Ser
   2130                2135                2140

tac aat aat att gtt gtc aac gta aag aca gct gtt gct gat aac ctc   6480
Tyr Asn Asn Ile Val Val Asn Val Lys Thr Ala Val Ala Asp Asn Leu
2145                2150                2155                2160

ctc ttt tat ctt gga agt gcc aaa ttt att gac ttt ctg gct ata gaa   6528
Leu Phe Tyr Leu Gly Ser Ala Lys Phe Ile Asp Phe Leu Ala Ile Glu
               2165                2170                2175

atg cgt aaa ggc aaa gtc agc ttc ctc tgg gat gtt gga tct gga gtt   6576
Met Arg Lys Gly Lys Val Ser Phe Leu Trp Asp Val Gly Ser Gly Val
           2180                2185                2190

gga cgt gta gag tac cca gat ttg act att gat gac tca tat tgg tac   6624
Gly Arg Val Glu Tyr Pro Asp Leu Thr Ile Asp Asp Ser Tyr Trp Tyr
       2195                2200                2205

cgt atc gta gca tca aga act ggg aga aat gga act att tct gtg aga   6672
Arg Ile Val Ala Ser Arg Thr Gly Arg Asn Gly Thr Ile Ser Val Arg
   2210                2215                2220

gcc ctg gat gga ccc aaa gcc agc att gtg ccc agc aca cac cat tcg   6720
Ala Leu Asp Gly Pro Lys Ala Ser Ile Val Pro Ser Thr His His Ser
2225                2230                2235                2240

acg tct cct cca ggg tac acg att cta gat gtg gat gca aat gca atg   6768
Thr Ser Pro Pro Gly Tyr Thr Ile Leu Asp Val Asp Ala Asn Ala Met
               2245                2250                2255

ctg ttt gtt ggt ggc ctg act ggg aaa tta aag aag gct gat gct gta   6816
Leu Phe Val Gly Gly Leu Thr Gly Lys Leu Lys Lys Ala Asp Ala Val
           2260                2265                2270

cgt gtg att aca ttc act ggc tgc atg gga gaa aca tac ttt gac aac   6864
Arg Val Ile Thr Phe Thr Gly Cys Met Gly Glu Thr Tyr Phe Asp Asn
       2275                2280                2285

aaa cct ata ggt ttg tgg aat ttc cga gaa aaa gaa ggt gac tgc aaa   6912
Lys Pro Ile Gly Leu Trp Asn Phe Arg Glu Lys Glu Gly Asp Cys Lys
   2290                2295                2300

gga tgc act gtc agt cct cag gtg gaa gat agt gag ggg act att caa   6960
Gly Cys Thr Val Ser Pro Gln Val Glu Asp Ser Glu Gly Thr Ile Gln
2305                2310                2315                2320

ttt gat gga gaa ggt tat gca ttg gtc agc cgt ccc att cgc tgg tac   7008
Phe Asp Gly Glu Gly Tyr Ala Leu Val Ser Arg Pro Ile Arg Trp Tyr
               2325                2330                2335

ccc aac atc tcc act gtc atg ttc aag ttc aga aca ttt tct tcg agt   7056
Pro Asn Ile Ser Thr Val Met Phe Lys Phe Arg Thr Phe Ser Ser Ser
           2340                2345                2350

gct ctt ctg atg tat ctt gcc aca cga gac ctg aga gat ttc atg agt   7104
Ala Leu Leu Met Tyr Leu Ala Thr Arg Asp Leu Arg Asp Phe Met Ser
       2355                2360                2365

gtg gag ctc act gat ggg cac ata aaa gtc agt tac gat ctg ggc tca   7152
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Val Glu Leu Thr Asp Gly His Ile Lys Val Ser Tyr Asp Leu Gly Ser
   2370                2375                2380

gga atg gct tcc gtt gtc agc aat caa aac cat aat gat ggg aaa tgg   7200
Gly Met Ala Ser Val Val Ser Asn Gln Asn His Asn Asp Gly Lys Trp
2385                2390                2395                2400

aaa tca ttc act ctg tca aga att caa aaa caa gcc aat ata tca att   7248
Lys Ser Phe Thr Leu Ser Arg Ile Gln Lys Gln Ala Asn Ile Ser Ile
               2405                2410                2415

gta gat ata gat act aat cag gag gag aat ata gca act tcg tct tct   7296
Val Asp Ile Asp Thr Asn Gln Glu Glu Asn Ile Ala Thr Ser Ser Ser
           2420                2425                2430

gga aac aac ttt ggt ctt gac ttg aaa gca gat gac aaa ata tat ttt   7344
Gly Asn Asn Phe Gly Leu Asp Leu Lys Ala Asp Asp Lys Ile Tyr Phe
       2435                2440                2445

ggt ggc ctg cca acg ctg aga aac ttg agt atg aaa gca agg cca gaa   7392
Gly Gly Leu Pro Thr Leu Arg Asn Leu Ser Met Lys Ala Arg Pro Glu
   2450                2455                2460

gta aat ctg aag aaa tat tcc ggc tgc ctc aaa gat att gaa att tca   7440
Val Asn Leu Lys Lys Tyr Ser Gly Cys Leu Lys Asp Ile Glu Ile Ser
2465                2470                2475                2480

aga act ccg tac aat ata ctc agt agt ccc gat tat gtt ggt gtt acc   7488
Arg Thr Pro Tyr Asn Ile Leu Ser Ser Pro Asp Tyr Val Gly Val Thr
               2485                2490                2495

aaa gga tgt tcc ctg gag aat gtt tac aca gtt agc ttt cct aag cct   7536
Lys Gly Cys Ser Leu Glu Asn Val Tyr Thr Val Ser Phe Pro Lys Pro
           2500                2505                2510

ggt ttt gtg gag ctc tcc cct gtg cca att gat gta gga aca gaa atc   7584
Gly Phe Val Glu Leu Ser Pro Val Pro Ile Asp Val Gly Thr Glu Ile
       2515                2520                2525

aac ctg tca ttc agc acc aag aat gag tcc ggc atc att ctt ttg gga   7632
Asn Leu Ser Phe Ser Thr Lys Asn Glu Ser Gly Ile Ile Leu Leu Gly
   2530                2535                2540

agt gga ggg aca cca gca cca cct agg aga aaa cga agg cag act gga   7680
Ser Gly Gly Thr Pro Ala Pro Pro Arg Arg Lys Arg Arg Gln Thr Gly
2545                2550                2555                2560

cag gcc tat tat gta ata ctc ctc aac agg ggc cgt ctg gaa gtg cat   7728
Gln Ala Tyr Tyr Val Ile Leu Leu Asn Arg Gly Arg Leu Glu Val His
               2565                2570                2575

ctc tcc aca ggg gca cga aca atg agg aaa att gtc atc aga cca gag   7776
Leu Ser Thr Gly Ala Arg Thr Met Arg Lys Ile Val Ile Arg Pro Glu
           2580                2585                2590

ccg aat ctg ttt cat gat gga aga gaa cat tcc gtt cat gta gag cga   7824
Pro Asn Leu Phe His Asp Gly Arg Glu His Ser Val His Val Glu Arg
       2595                2600                2605

act aga ggc atc ttt aca gtt caa gtg gat gaa aac aga aga tac atg   7872
Thr Arg Gly Ile Phe Thr Val Gln Val Asp Glu Asn Arg Arg Tyr Met
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   2610                2615                2620

caa aac ctg aca gtt gaa cag cct atc gaa gtt aaa aag ctt ttc gtt   7920
Gln Asn Leu Thr Val Glu Gln Pro Ile Glu Val Lys Lys Leu Phe Val
2625                2630                2635                2640

ggg ggt gct cca cct gaa ttt caa cct tcc cca ctc aga aat att cct   7968
Gly Gly Ala Pro Pro Glu Phe Gln Pro Ser Pro Leu Arg Asn Ile Pro
                2645                2650                2655

cct ttt gaa ggc tgc ata tgg aat ctt gtt att aac tct gtc ccc atg   8016
Pro Phe Glu Gly Cys Ile Trp Asn Leu Val Ile Asn Ser Val Pro Met
            2660                2665                2670

gac ttt gca agg cct gtg tcc ttc aaa aat gct gac att ggt cgc tgt   8064
Asp Phe Ala Arg Pro Val Ser Phe Lys Asn Ala Asp Ile Gly Arg Cys
        2675                2680                2685

gcc cat cag aaa ctc cgt gaa gat gaa gat gga gca gct cca gct gaa   8112
Ala His Gln Lys Leu Arg Glu Asp Glu Asp Gly Ala Ala Pro Ala Glu
    2690                2695                2700

ata gtt atc cag cct gag cca gtt ccc acc cca gcc ttt cct acg ccc   8160
Ile Val Ile Gln Pro Glu Pro Val Pro Thr Pro Ala Phe Pro Thr Pro
2705                2710                2715                2720

acc cca gtt ctg aca cat ggt cct tgt gct gca gaa tca gaa cca gct   8208
Thr Pro Val Leu Thr His Gly Pro Cys Ala Ala Glu Ser Glu Pro Ala
                2725                2730                2735

ctt ttg ata ggg agc aag cag ttc ggg ctt tca aga aac agt cac att   8256
Leu Leu Ile Gly Ser Lys Gln Phe Gly Leu Ser Arg Asn Ser His Ile
            2740                2745                2750

gca att gca ttt gat gac acc aaa gtt aaa aac cgt ctc aca att gag   8304
Ala Ile Ala Phe Asp Asp Thr Lys Val Lys Asn Arg Leu Thr Ile Glu
        2755                2760                2765

ttg gaa gta aga acc gaa gct gaa tcc ggc ttg ctt ttt tac atg gct   8352
Leu Glu Val Arg Thr Glu Ala Glu Ser Gly Leu Leu Phe Tyr Met Ala
    2770                2775                2780

gcg atc aat cat gct gat ttt gca aca gtt cag ctg aga aat gga ttg   8400
Ala Ile Asn His Ala Asp Phe Ala Thr Val Gln Leu Arg Asn Gly Leu
2785                2790                2795                2800

ccc tac ttc agc tat gac ttg ggg agt ggg gac acc cac acc atg atc   8448
Pro Tyr Phe Ser Tyr Asp Leu Gly Ser Gly Asp Thr His Thr Met Ile
                2805                2810                2815

ccc acc aaa atc aat gat ggc cag tgg cac aag att aag ata atg aga   8496
Pro Thr Lys Ile Asn Asp Gly Gln Trp His Lys Ile Lys Ile Met Arg
            2820                2825                2830

agt aag caa gaa gga att ctt tat gta gat ggg gct tcc aac aga acc   8544
Ser Lys Gln Glu Gly Ile Leu Tyr Val Asp Gly Ala Ser Asn Arg Thr
        2835                2840                2845

atc agt ccc aaa aaa gcc gac atc ctg gat gtc gtg gga atg ctg tat   8592
Ile Ser Pro Lys Lys Ala Asp Ile Leu Asp Val Val Gly Met Leu Tyr
    2850                2855                2860
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gtt ggt ggg tta ccc atc aac tac act acc cga aga att ggt cca gtg   8640
Val Gly Gly Leu Pro Ile Asn Tyr Thr Thr Arg Arg Ile Gly Pro Val
2865                2870                2875                2880

acc tat agc att gat ggc tgc gtc agg aat ctc cac atg gca gag gcc   8688
Thr Tyr Ser Ile Asp Gly Cys Val Arg Asn Leu His Met Ala Glu Ala
                2885                2890                2895

cct gcc gat ctg gaa caa ccc acc tcc agc ttc cat gtt ggg aca tgt   8736
Pro Ala Asp Leu Glu Gln Pro Thr Ser Ser Phe His Val Gly Thr Cys
            2900                2905                2910

ttt gca aat gct cag agg gga aca tat ttt gac gga acc ggt ttt gcc   8784
Phe Ala Asn Ala Gln Arg Gly Thr Tyr Phe Asp Gly Thr Gly Phe Ala
        2915                2920                2925

aaa gca gtt ggt gga ttc aaa gtg gga ttg gac ctt ctt gta gaa ttt   8832
Lys Ala Val Gly Gly Phe Lys Val Gly Leu Asp Leu Leu Val Glu Phe
    2930                2935                2940

gaa ttc gcg aca act aca acg act gga gtt ctt ctg ggg atc agt agt   8880
Glu Phe Ala Thr Thr Thr Thr Thr Gly Val Leu Leu Gly Ile Ser Ser
2945                2950                2955                2960

caa aaa atg gat gga atg ggt att gaa atg att gat gaa aag ttg atg   8928
Gln Lys Met Asp Gly Met Gly Ile Glu Met Ile Asp Glu Lys Leu Met
                2965                2970                2975

ttt cat gtg gac aat ggt gcg ggc aga ttc act gct gtc tat gat gct   8976
Phe His Val Asp Asn Gly Ala Gly Arg Phe Thr Ala Val Tyr Asp Ala
            2980                2985                2990

ggg gtt cca ggg cat ttg tgt gat gga caa tgg cat aaa gtc act gcc   9024
Gly Val Pro Gly His Leu Cys Asp Gly Gln Trp His Lys Val Thr Ala
        2995                3000                3005

aac aag atc aaa cac cgc att gag ctc aca gtc gat ggg aac cag gtg   9072
Asn Lys Ile Lys His Arg Ile Glu Leu Thr Val Asp Gly Asn Gln Val
    3010                3015                3020

gaa gcc caa agc cca aac cca gca tct aca tca gct gac aca aat gac   9120
Glu Ala Gln Ser Pro Asn Pro Ala Ser Thr Ser Ala Asp Thr Asn Asp
3025                3030                3035                3040

cct gtg ttt gtt gga ggc ttc cca gat gac ctc aag cag ttt ggc cta   9168
Pro Val Phe Val Gly Gly Phe Pro Asp Asp Leu Lys Gln Phe Gly Leu
                3045                3050                3055

aca acc agt att ccg ttc cga ggt tgc atc aga tcc ctg aag ctc acc   9216
Thr Thr Ser Ile Pro Phe Arg Gly Cys Ile Arg Ser Leu Lys Leu Thr
            3060                3065                3070

aaa ggc aca ggc aag cca ctg gag gtt aat ttt gcc aag gcc ctg gaa   9264
Lys Gly Thr Gly Lys Pro Leu Glu Val Asn Phe Ala Lys Ala Leu Glu
        3075                3080                3085

ctg aggggcgttc aacctgtatc atgcccagcc aactaataaa aataagtgta        9317
Leu

accccaggaa gagtctgtca aaacaagtat atcaagtaaa acaaacaaat atattttacc 9377
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<213> Homo sapiens

<400> 4

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Gln Arg Pro Gln Gln Gln Arg Gln Ser Gln Ala His Gln Gln Arg Gly
  1               5                  10                  15

Leu Phe Pro Ala Val Leu Asn Leu Ala Ser Asn Ala Leu Ile Thr Thr
             20                  25                  30

Asn Ala Thr Cys Gly Glu Lys Gly Pro Glu Met Tyr Cys Lys Leu Val
         35                  40                  45

Glu His Val Pro Gly Gln Pro Val Arg Asn Pro Gln Cys Arg Ile Cys
     50                  55                  60

Asn Gln Asn Ser Ser Asn Pro Asn Gln Arg His Pro Ile Thr Asn Ala
 65                  70                  75                  80

Ile Asp Gly Lys Asn Thr Trp Trp Gln Ser Pro Ser Ile Lys Asn Gly
                 85                  90                  95

Ile Glu Tyr His Tyr Val Thr Ile Thr Leu Asp Leu Gln Gln Val Phe
            100                 105                 110

Gln Ile Ala Tyr Val Ile Val Lys Ala Ala Asn Ser Pro Arg Pro Gly
        115                 120                 125

Asn Trp Ile Leu Glu Arg Ser Leu Asp Asp Val Glu Tyr Lys Pro Trp
    130                 135                 140

Gln Tyr His Ala Val Thr Asp Thr Glu Cys Leu Thr Leu Tyr Asn Ile
145                 150                 155                 160

Tyr Pro Arg Thr Gly Pro Pro Ser Tyr Ala Lys Asp Asp Glu Val Ile
                165                 170                 175

Cys Thr Ser Phe Tyr Ser Lys Ile His Pro Leu Glu Asn Gly Glu Ile
            180                 185                 190

His Ile Ser Leu Ile Asn Gly Arg Pro Ser Ala Asp Asp Pro Ser Pro
        195                 200                 205

Glu Leu Leu Glu Phe Thr Ser Ala Arg Tyr Ile Arg Leu Arg Phe Gln
    210                 215                 220

Arg Ile Arg Thr Leu Asn Ala Asp Leu Met Met Phe Ala His Lys Asp
225                 230                 235                 240

Pro Arg Glu Ile Asp Pro Ile Val Thr Arg Arg Tyr Tyr Tyr Ser Val
                245                 250                 255

Lys Asp Ile Ser Val Gly Gly Met Cys Ile Cys Tyr Gly His Ala Arg
            260                 265                 270
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Ala Cys Pro Leu Asp Pro Ala Thr Asn Lys Ser Arg Cys Glu Cys Glu
        275                 280                 285

His Asn Thr Cys Gly Asp Ser Cys Asp Gln Cys Cys Pro Gly Phe His
    290                 295                 300

Gln Lys Pro Trp Arg Ala Gly Thr Phe Leu Thr Lys Thr Glu Cys Glu
305                 310                 315                 320

Ala Cys Asn Cys His Gly Lys Ala Glu Glu Cys Tyr Tyr Asp Glu Asn
                325                 330                 335

Val Ala Arg Arg Asn Leu Ser Leu Asn Ile Arg Gly Lys Tyr Ile Gly
            340                 345                 350

Gly Gly Val Cys Ile Asn Cys Thr Gln Asn Thr Ala Gly Ile Asn Cys
        355                 360                 365

Glu Thr Cys Thr Asp Gly Phe Phe Arg Pro Lys Gly Val Ser Pro Asn
    370                 375                 380

Tyr Pro Arg Pro Cys Gln Pro Cys His Cys Asp Pro Ile Gly Ser Leu
385                 390                 395                 400

Asn Glu Val Cys Val Lys Asp Glu Lys His Ala Arg Arg Gly Leu Ala
                405                 410                 415

Pro Gly Ser Cys His Cys Lys Thr Gly Phe Gly Gly Val Ser Cys Asp
            420                 425                 430

Arg Cys Ala Arg Gly Tyr Thr Gly Tyr Pro Asp Cys Lys Ala Cys Asn
        435                 440                 445

Cys Ser Gly Leu Gly Ser Lys Asn Glu Asp Pro Cys Phe Gly Pro Cys
    450                 455                 460

Ile Cys Lys Glu Asn Val Glu Gly Gly Asp Cys Ser Arg Cys Lys Ser
465                 470                 475                 480

Gly Phe Phe Asn Leu Gln Glu Asp Asn Trp Lys Gly Cys Asp Glu Cys
                485                 490                 495

Phe Cys Ser Gly Val Ser Asn Arg Cys Gln Ser Ser Tyr Trp Thr Tyr
            500                 505                 510

Gly Lys Ile Gln Asp Met Ser Gly Trp Tyr Leu Thr Asp Leu Pro Gly
        515                 520                 525

Arg Ile Arg Val Ala Pro Gln Gln Asp Asp Leu Asp Ser Pro Gln Gln
    530                 535                 540

Ile Ser Ile Ser Asn Ala Glu Ala Arg Gln Ala Leu Pro His Ser Tyr
545                 550                 555                 560

Tyr Trp Ser Ala Pro Ala Pro Tyr Leu Gly Asn Lys Leu Pro Ala Val
                565                 570                 575

Gly Gly Gln Leu Thr Phe Thr Ile Ser Tyr Asp Leu Glu Glu Glu Glu
            580                 585                 590

Glu Asp Thr Glu Arg Val Leu Gln Leu Met Ile Ile Leu Glu Gly Asn
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595 600 605

Asp Leu Ser Ile Ser Thr Ala Gln Asp Glu Val Tyr Leu His Pro Ser
610 615 620

Glu Glu His Thr Asn Val Leu Leu Leu Lys Glu Glu Ser Phe Thr Ile
625 630 635 640

His Gly Thr His Phe Pro Val Arg Arg Lys Glu Phe Met Thr Val Leu
645 650 655

Ala Asn Leu Lys Arg Val Leu Leu Gln Ile Thr Tyr Ser Phe Gly Met
660 665 670

Asp Ala Ile Phe Arg Leu Ser Ser Val Asn Leu Glu Ser Ala Val Ser
675 680 685

Tyr Pro Thr Asp Gly Ser Ile Ala Ala Ala Val Glu Val Cys Gln Cys
690 695 700

Pro Pro Gly Tyr Thr Gly Ser Ser Cys Glu Ser Cys Trp Pro Arg His
705 710 715 720

Arg Arg Val Asn Gly Thr Ile Phe Gly Gly Ile Cys Glu Pro Cys Gln
725 730 735

Cys Phe Gly His Ala Glu Ser Cys Asp Asp Val Thr Gly Glu Cys Leu
740 745 750

Asn Cys Lys Asp His Thr Gly Gly Pro Tyr Cys Asp Lys Cys Leu Pro
755 760 765

Gly Phe Tyr Gly Glu Pro Thr Lys Gly Thr Ser Glu Asp Cys Gln Pro
770 775 780

Cys Ala Cys Pro Leu Asn Ile Pro Ser Asn Asn Phe Ser Pro Thr Cys
785 790 795 800

His Leu Asp Arg Ser Leu Gly Leu Ile Cys Asp Gly Cys Pro Val Gly
805 810 815

Tyr Thr Gly Pro Arg Cys Glu Arg Cys Ala Glu Gly Tyr Phe Gly Gln
820 825 830

Pro Ser Val Pro Gly Gly Ser Cys Gln Pro Cys Gln Cys Asn Asp Asn
835 840 845

Leu Asp Phe Ser Ile Pro Gly Ser Cys Asp Ser Leu Ser Gly Ser Cys
850 855 860

Leu Ile Cys Lys Pro Gly Thr Thr Gly Arg Tyr Cys Glu Leu Cys Ala
865 870 875 880

Asp Gly Tyr Phe Gly Asp Ala Val Asp Ala Lys Asn Cys Gln Pro Cys
885 890 895

Arg Cys Asn Ala Gly Gly Ser Phe Ser Glu Val Cys His Ser Gln Thr
900 905 910

Gly Gln Cys Glu Cys Arg Ala Asn Val Gln Gly Gln Arg Cys Asp Lys
915 920 925

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Cys Lys Ala Gly Thr Phe Gly Leu Gln Ser Ala Arg Gly Cys Val Pro
    930                 935                 940

Cys Asn Cys Asn Ser Phe Gly Ser Lys Ser Phe Asp Cys Glu Glu Ser
945                 950                 955                 960

Gly Gln Cys Trp Cys Gln Pro Gly Val Thr Gly Lys Lys Cys Asp Arg
                965                 970                 975

Cys Ala His Gly Tyr Phe Asn Phe Gln Glu Gly Gly Cys Thr Ala Cys
            980                 985                 990

Glu Cys Ser His Leu Gly Asn Asn Cys Asp Pro Lys Thr Gly Arg Cys
        995                1000                1005

Ile Cys Pro Pro Asn Thr Ile Gly Glu Lys Cys Ser Lys Cys Ala Pro
   1010                1015                1020

Asn Thr Trp Gly His Ser Ile Thr Thr Gly Cys Lys Ala Cys Asn Cys
1025                1030                1035                1040

Ser Thr Val Gly Ser Leu Asp Phe Gln Cys Asn Val Asn Thr Gly Gln
                1045                1050                1055

Cys Asn Cys His Pro Lys Phe Ser Gly Ala Lys Cys Thr Glu Cys Ser
            1060                1065                1070

Arg Gly His Trp Asn Tyr Pro Arg Cys Asn Leu Cys Asp Cys Phe Leu
        1075                1080                1085

Pro Gly Thr Asp Ala Thr Thr Cys Asp Ser Glu Thr Lys Lys Cys Ser
    1090                1095                1100

Cys Ser Asp Gln Thr Gly Gln Cys Thr Cys Lys Val Asn Val Glu Gly
1105                1110                1115                1120

Ile His Cys Asp Arg Cys Arg Pro Gly Lys Phe Gly Leu Asp Ala Lys
                1125                1130                1135

Asn Pro Leu Gly Cys Ser Ser Cys Tyr Cys Phe Gly Thr Thr Thr Gln
            1140                1145                1150

Cys Ser Glu Ala Lys Gly Leu Ile Arg Thr Trp Val Thr Leu Lys Ala
        1155                1160                1165

Glu Gln Thr Ile Leu Pro Leu Val Asp Glu Ala Leu Gln His Thr Thr
    1170                1175                1180

Thr Lys Gly Ile Val Phe Gln His Pro Glu Ile Val Ala His Met Asp
1185                1190                1195                1200

Leu Met Arg Glu Asp Leu His Leu Glu Pro Phe Tyr Trp Lys Leu Pro
                1205                1210                1215

Glu Gln Phe Glu Gly Lys Lys Leu Met Ala Tyr Gly Gly Lys Leu Lys
            1220                1225                1230

Tyr Ala Ile Tyr Phe Glu Ala Arg Glu Glu Thr Gly Phe Ser Thr Tyr
        1235                1240                1245
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Asn Pro Gln Val Ile Ile Arg Gly Gly Thr Pro Thr His Ala Arg Ile
  1250                1255                1260

Ile Val Arg His Met Ala Ala Pro Leu Ile Gly Gln Leu Thr Arg His
1265                1270                1275                1280

Glu Ile Glu Met Thr Glu Lys Glu Trp Lys Tyr Tyr Gly Asp Asp Pro
                1285                1290                1295

Arg Val His Arg Thr Val Thr Arg Glu Asp Phe Leu Asp Ile Leu Tyr
            1300                1305                1310

Asp Ile His Tyr Ile Leu Ile Lys Ala Thr Tyr Gly Asn Phe Met Arg
        1315                1320                1325

Gln Ser Arg Ile Ser Glu Ile Ser Met Glu Val Ala Glu Gln Gly Arg
  1330                1335                1340

Gly Thr Thr Met Thr Pro Pro Ala Asp Leu Ile Glu Lys Cys Asp Cys
1345                1350                1355                1360

Pro Leu Gly Tyr Ser Gly Leu Ser Cys Glu Ala Cys Leu Pro Gly Phe
                1365                1370                1375

Tyr Arg Leu Arg Ser Gln Pro Gly Gly Arg Thr Pro Gly Pro Thr Leu
            1380                1385                1390

Gly Thr Cys Val Pro Cys Gln Cys Asn Gly His Ser Ser Leu Cys Asp
        1395                1400                1405

Pro Glu Thr Ser Ile Cys Gln Asn Cys Gln His His Thr Ala Gly Asp
  1410                1415                1420

Phe Cys Glu Arg Cys Ala Leu Gly Tyr Tyr Gly Ile Val Lys Gly Leu
1425                1430                1435                1440

Pro Asn Asp Cys Gln Gln Cys Ala Cys Pro Leu Ile Ser Ser Ser Asn
                1445                1450                1455

Asn Phe Ser Pro Ser Cys Val Ala Glu Gly Leu Asp Asp Tyr Arg Cys
            1460                1465                1470

Thr Ala Cys Pro Arg Gly Tyr Glu Gly Gln Tyr Cys Glu Arg Cys Ala
        1475                1480                1485

Pro Gly Tyr Thr Gly Ser Pro Gly Asn Pro Gly Gly Ser Cys Gln Glu
  1490                1495                1500

Cys Glu Cys Asp Pro Tyr Gly Ser Leu Pro Val Pro Cys Asp Pro Val
1505                1510                1515                1520

Thr Gly Phe Cys Thr Cys Arg Pro Gly Ala Thr Gly Arg Lys Cys Asp
                1525                1530                1535

Gly Cys Lys His Trp His Ala Arg Glu Gly Trp Glu Cys Val Phe Cys
            1540                1545                1550

Gly Asp Glu Cys Thr Gly Leu Leu Leu Gly Asp Leu Ala Arg Leu Glu
        1555                1560                1565

Gln Met Val Met Ser Ile Asn Leu Thr Gly Pro Leu Pro Ala Pro Tyr
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   1570                1575                1580

Lys Met Leu Tyr Gly Leu Glu Asn Met Thr Gln Glu Leu Lys His Leu
1585                1590                1595                1600

Leu Ser Pro Gln Arg Ala Pro Glu Arg Leu Ile Gln Leu Ala Glu Gly
                1605                1610                1615

Asn Leu Asn Thr Leu Val Thr Glu Met Asn Glu Leu Leu Thr Arg Ala
            1620                1625                1630

Thr Lys Val Thr Ala Asp Gly Glu Gln Thr Gly Gln Asp Ala Glu Arg
        1635                1640                1645

Thr Asn Thr Arg Ala Lys Ser Leu Gly Glu Phe Ile Lys Glu Leu Ala
    1650                1655                1660

Arg Asp Ala Glu Ala Val Asn Glu Lys Ala Ile Lys Leu Asn Glu Thr
1665                1670                1675                1680

Leu Gly Thr Arg Asp Glu Ala Phe Glu Arg Asn Leu Glu Gly Leu Gln
                1685                1690                1695

Lys Glu Ile Asp Gln Met Ile Lys Glu Leu Arg Arg Lys Asn Leu Glu
            1700                1705                1710

Thr Gln Lys Glu Ile Ala Glu Asp Glu Leu Val Ala Ala Glu Ala Leu
        1715                1720                1725

Leu Lys Lys Val Lys Lys Leu Phe Gly Glu Ser Arg Gly Glu Asn Glu
    1730                1735                1740

Glu Met Glu Lys Asp Leu Arg Glu Lys Leu Ala Asp Tyr Lys Asn Lys
1745                1750                1755                1760

Val Asp Asp Ala Trp Asp Leu Leu Arg Glu Ala Thr Asp Lys Ile Arg
                1765                1770                1775

Glu Ala Asn Arg Leu Phe Ala Val Asn Gln Lys Asn Met Thr Ala Leu
            1780                1785                1790

Glu Lys Lys Lys Glu Ala Val Glu Ser Gly Lys Arg Gln Ile Glu Asn
        1795                1800                1805

Thr Leu Lys Glu Gly Asn Asp Ile Leu Asp Glu Ala Asn Arg Leu Ala
    1810                1815                1820

Asp Glu Ile Asn Ser Ile Ile Asp Tyr Val Glu Asp Ile Gln Thr Lys
1825                1830                1835                1840

Leu Pro Pro Met Ser Glu Glu Leu Asn Asp Lys Ile Asp Asp Leu Ser
                1845                1850                1855

Gln Glu Ile Lys Asp Arg Lys Leu Ala Glu Lys Val Ser Gln Ala Glu
            1860                1865                1870

Ser His Ala Ala Gln Leu Asn Asp Ser Ser Ala Val Leu Asp Gly Ile
        1875                1880                1885

Leu Asp Glu Ala Lys Asn Ile Ser Phe Asn Ala Thr Ala Ala Phe Lys
    1890                1895                1900
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Ala Tyr Ser Asn Ile Lys Asp Tyr Ile Asp Glu Ala Glu Lys Val Ala
1905                1910                1915                1920

Lys Glu Ala Lys Asp Leu Ala His Glu Ala Thr Lys Leu Ala Thr Gly
                1925                1930                1935

Pro Arg Gly Leu Leu Lys Glu Asp Ala Lys Gly Cys Leu Gln Lys Ser
            1940                1945                1950

Phe Arg Ile Leu Asn Glu Ala Lys Lys Leu Ala Asn Asp Val Lys Glu
        1955                1960                1965

Asn Glu Asp His Leu Asn Gly Leu Lys Thr Arg Ile Glu Asn Ala Asp
    1970                1975                1980

Ala Arg Asn Gly Asp Leu Leu Arg Thr Leu Asn Asp Thr Leu Gly Lys
1985                1990                1995                2000

Leu Ser Ala Ile Pro Asn Asp Thr Ala Ala Lys Leu Gln Ala Val Lys
                2005                2010                2015

Asp Lys Ala Arg Gln Ala Asn Asp Thr Ala Lys Asp Val Leu Ala Gln
            2020                2025                2030

Ile Thr Glu Leu His Gln Asn Leu Asp Gly Leu Lys Lys Asn Tyr Asn
        2035                2040                2045

Lys Leu Ala Asp Ser Val Ala Lys Thr Asn Ala Val Val Lys Asp Pro
    2050                2055                2060

Ser Lys Asn Lys Ile Ile Ala Asp Ala Asp Ala Thr Val Lys Asn Leu
2065                2070                2075                2080

Glu Gln Glu Ala Asp Arg Leu Ile Asp Lys Leu Lys Pro Ile Lys Glu
                2085                2090                2095

Leu Glu Asp Asn Leu Lys Lys Asn Ile Ser Glu Ile Lys Glu Leu Ile
            2100                2105                2110

Asn Gln Ala Arg Lys Gln Ala Asn Ser Ile Lys Val Ser Val Ser Ser
        2115                2120                2125

Gly Gly Asp Cys Ile Arg Thr Tyr Lys Pro Glu Ile Lys Lys Gly Ser
    2130                2135                2140

Tyr Asn Asn Ile Val Val Asn Val Lys Thr Ala Val Ala Asp Asn Leu
2145                2150                2155                2160

Leu Phe Tyr Leu Gly Ser Ala Lys Phe Ile Asp Phe Leu Ala Ile Glu
                2165                2170                2175

Met Arg Lys Gly Lys Val Ser Phe Leu Trp Asp Val Gly Ser Gly Val
            2180                2185                2190

Gly Arg Val Glu Tyr Pro Asp Leu Thr Ile Asp Asp Ser Tyr Trp Tyr
        2195                2200                2205

Arg Ile Val Ala Ser Arg Thr Gly Arg Asn Gly Thr Ile Ser Val Arg
    2210                2215                2220
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Ala Leu Asp Gly Pro Lys Ala Ser Ile Val Pro Ser Thr His His Ser
2225                2230                2235                2240

Thr Ser Pro Pro Gly Tyr Thr Ile Leu Asp Val Asp Ala Asn Ala Met
                2245                2250                2255

Leu Phe Val Gly Gly Leu Thr Gly Lys Leu Lys Lys Ala Asp Ala Val
            2260                2265                2270

Arg Val Ile Thr Phe Thr Gly Cys Met Gly Glu Thr Tyr Phe Asp Asn
        2275                2280                2285

Lys Pro Ile Gly Leu Trp Asn Phe Arg Glu Lys Glu Gly Asp Cys Lys
    2290                2295                2300

Gly Cys Thr Val Ser Pro Gln Val Glu Asp Ser Glu Gly Thr Ile Gln
2305                2310                2315                2320

Phe Asp Gly Glu Gly Tyr Ala Leu Val Ser Arg Pro Ile Arg Trp Tyr
                2325                2330                2335

Pro Asn Ile Ser Thr Val Met Phe Lys Phe Arg Thr Phe Ser Ser Ser
            2340                2345                2350

Ala Leu Leu Met Tyr Leu Ala Thr Arg Asp Leu Arg Asp Phe Met Ser
        2355                2360                2365

Val Glu Leu Thr Asp Gly His Ile Lys Val Ser Tyr Asp Leu Gly Ser
    2370                2375                2380

Gly Met Ala Ser Val Val Ser Asn Gln Asn His Asn Asp Gly Lys Trp
2385                2390                2395                2400

Lys Ser Phe Thr Leu Ser Arg Ile Gln Lys Gln Ala Asn Ile Ser Ile
                2405                2410                2415

Val Asp Ile Asp Thr Asn Gln Glu Glu Asn Ile Ala Thr Ser Ser Ser
            2420                2425                2430

Gly Asn Asn Phe Gly Leu Asp Leu Lys Ala Asp Asp Lys Ile Tyr Phe
        2435                2440                2445

Gly Gly Leu Pro Thr Leu Arg Asn Leu Ser Met Lys Ala Arg Pro Glu
    2450                2455                2460

Val Asn Leu Lys Lys Tyr Ser Gly Cys Leu Lys Asp Ile Glu Ile Ser
2465                2470                2475                2480

Arg Thr Pro Tyr Asn Ile Leu Ser Ser Pro Asp Tyr Val Gly Val Thr
                2485                2490                2495

Lys Gly Cys Ser Leu Glu Asn Val Tyr Thr Val Ser Phe Pro Lys Pro
            2500                2505                2510

Gly Phe Val Glu Leu Ser Pro Val Pro Ile Asp Val Gly Thr Glu Ile
        2515                2520                2525

Asn Leu Ser Phe Ser Thr Lys Asn Glu Ser Gly Ile Ile Leu Leu Gly
    2530                2535                2540

Ser Gly Gly Thr Pro Ala Pro Pro Arg Arg Lys Arg Arg Gln Thr Gly
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2545                2550                2555                2560

Gln Ala Tyr Tyr Val Ile Leu Leu Asn Arg Gly Arg Leu Glu Val His
                2565                2570                2575

Leu Ser Thr Gly Ala Arg Thr Met Arg Lys Ile Val Ile Arg Pro Glu
            2580                2585                2590

Pro Asn Leu Phe His Asp Gly Arg Glu His Ser Val His Val Glu Arg
        2595                2600                2605

Thr Arg Gly Ile Phe Thr Val Gln Val Asp Glu Asn Arg Arg Tyr Met
    2610                2615                2620

Gln Asn Leu Thr Val Glu Gln Pro Ile Glu Val Lys Lys Leu Phe Val
2625                2630                2635                2640

Gly Gly Ala Pro Pro Glu Phe Gln Pro Ser Pro Leu Arg Asn Ile Pro
                2645                2650                2655

Pro Phe Glu Gly Cys Ile Trp Asn Leu Val Ile Asn Ser Val Pro Met
            2660                2665                2670

Asp Phe Ala Arg Pro Val Ser Phe Lys Asn Ala Asp Ile Gly Arg Cys
        2675                2680                2685

Ala His Gln Lys Leu Arg Glu Asp Glu Asp Gly Ala Ala Pro Ala Glu
    2690                2695                2700

Ile Val Ile Gln Pro Glu Pro Val Pro Thr Pro Ala Phe Pro Thr Pro
2705                2710                2715                2720

Thr Pro Val Leu Thr His Gly Pro Cys Ala Ala Glu Ser Glu Pro Ala
                2725                2730                2735

Leu Leu Ile Gly Ser Lys Gln Phe Gly Leu Ser Arg Asn Ser His Ile
            2740                2745                2750

Ala Ile Ala Phe Asp Asp Thr Lys Val Lys Asn Arg Leu Thr Ile Glu
        2755                2760                2765

Leu Glu Val Arg Thr Glu Ala Glu Ser Gly Leu Leu Phe Tyr Met Ala
    2770                2775                2780

Ala Ile Asn His Ala Asp Phe Ala Thr Val Gln Leu Arg Asn Gly Leu
2785                2790                2795                2800

Pro Tyr Phe Ser Tyr Asp Leu Gly Ser Gly Asp Thr His Thr Met Ile
                2805                2810                2815

Pro Thr Lys Ile Asn Asp Gly Gln Trp His Lys Ile Lys Ile Met Arg
            2820                2825                2830

Ser Lys Gln Glu Gly Ile Leu Tyr Val Asp Gly Ala Ser Asn Arg Thr
        2835                2840                2845

Ile Ser Pro Lys Lys Ala Asp Ile Leu Asp Val Val Gly Met Leu Tyr
    2850                2855                2860

Val Gly Gly Leu Pro Ile Asn Tyr Thr Thr Arg Arg Ile Gly Pro Val
2865                2870                2875                2880
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Thr Tyr Ser Ile Asp Gly Cys Val Arg Asn Leu His Met Ala Glu Ala
                2885                2890                2895

Pro Ala Asp Leu Glu Gln Pro Thr Ser Ser Phe His Val Gly Thr Cys
            2900                2905                2910

Phe Ala Asn Ala Gln Arg Gly Thr Tyr Phe Asp Gly Thr Gly Phe Ala
        2915                2920                2925

Lys Ala Val Gly Gly Phe Lys Val Gly Leu Asp Leu Leu Val Glu Phe
    2930                2935                2940

Glu Phe Ala Thr Thr Thr Thr Thr Gly Val Leu Leu Gly Ile Ser Ser
2945                2950                2955                2960

Gln Lys Met Asp Gly Met Gly Ile Glu Met Ile Asp Glu Lys Leu Met
                2965                2970                2975

Phe His Val Asp Asn Gly Ala Gly Arg Phe Thr Ala Val Tyr Asp Ala
            2980                2985                2990

Gly Val Pro Gly His Leu Cys Asp Gly Gln Trp His Lys Val Thr Ala
        2995                3000                3005

Asn Lys Ile Lys His Arg Ile Glu Leu Thr Val Asp Gly Asn Gln Val
    3010                3015                3020

Glu Ala Gln Ser Pro Asn Pro Ala Ser Thr Ser Ala Asp Thr Asn Asp
3025                3030                3035                3040

Pro Val Phe Val Gly Gly Phe Pro Asp Asp Leu Lys Gln Phe Gly Leu
                3045                3050                3055

Thr Thr Ser Ile Pro Phe Arg Gly Cys Ile Arg Ser Leu Lys Leu Thr
            3060                3065                3070

Lys Gly Thr Gly Lys Pro Leu Glu Val Asn Phe Ala Lys Ala Leu Glu
        3075                3080                3085

Leu
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gcc gcc ggg gtc ctc ctc ctt ctg ctg ctc tcc gga ggc ctc ggg ggc   106
Ala Ala Gly Val Leu Leu Leu Leu Leu Ser Gly Gly Leu Gly Gly
  5                  10                  15

gta cag gcg cag cgg ccg cag cag cag cgg cag tca cag gca cat cag   154
Val Gln Ala Gln Arg Pro Gln Gln Gln Arg Gln Ser Gln Ala His Gln
 20                  25                  30                  35

caa aga ggt tta ttc cct gct gtc ctg aat ctt gct tct aat gct ctt   202
Gln Arg Gly Leu Phe Pro Ala Val Leu Asn Leu Ala Ser Asn Ala Leu
             40                  45                  50

atc acg acc aat gca aca tgt gga gaa aaa gga cct gaa atg tac tgc   250
Ile Thr Thr Asn Ala Thr Cys Gly Glu Lys Gly Pro Glu Met Tyr Cys
         55                  60                  65

aaa ttg gta gaa cat gtc cct ggg cag cct gtg agg aac ccg cag tgt   298
Lys Leu Val Glu His Val Pro Gly Gln Pro Val Arg Asn Pro Gln Cys
     70                  75                  80

cga atc tgc aat caa aac agc agc aat cca aac cag aga cac ccg att   346
Arg Ile Cys Asn Gln Asn Ser Ser Asn Pro Asn Gln Arg His Pro Ile
  85                  90                  95

aca aat gct att gat gga aag aac act tgg tgg cag agt ccc agt att   394
Thr Asn Ala Ile Asp Gly Lys Asn Thr Trp Trp Gln Ser Pro Ser Ile
100                 105                 110                 115

aag aat gga atc gaa tac cat tat gtg aca att aca ctg gat tta cag   442
Lys Asn Gly Ile Glu Tyr His Tyr Val Thr Ile Thr Leu Asp Leu Gln
             120                 125                 130

cag gtg ttc cag atc gcg tat gtg att gtg aag gca gct aac tcc ccc   490
Gln Val Phe Gln Ile Ala Tyr Val Ile Val Lys Ala Ala Asn Ser Pro
         135                 140                 145

cgg cct gga aac tgg att ttg gaa cgc tct ctt gat gat gtt gaa tac   538
Arg Pro Gly Asn Trp Ile Leu Glu Arg Ser Leu Asp Asp Val Glu Tyr
     150                 155                 160

aag ccc tgg cag tat cat gct gtg aca gac acg gag tgc cta acg ctt   586
Lys Pro Trp Gln Tyr His Ala Val Thr Asp Thr Glu Cys Leu Thr Leu
 165                 170                 175

tac aat att tat ccc cgc act ggg cca ccg tca tat gcc aaa gat gat   634
Tyr Asn Ile Tyr Pro Arg Thr Gly Pro Pro Ser Tyr Ala Lys Asp Asp
180                 185                 190                 195

gag gtc atc tgc act tca ttt tac tcc aag ata cac ccc tta gaa aat   682
Glu Val Ile Cys Thr Ser Phe Tyr Ser Lys Ile His Pro Leu Glu Asn
             200                 205                 210

gga gag att cac atc tct tta atc aat ggg aga cca agt gcc gat gat   730
Gly Glu Ile His Ile Ser Leu Ile Asn Gly Arg Pro Ser Ala Asp Asp
         215                 220                 225

cct tct cca gaa ctg cta gaa ttt acc tcc gct cgc tat att cgc ctg   778
Pro Ser Pro Glu Leu Leu Glu Phe Thr Ser Ala Arg Tyr Ile Arg Leu
     230                 235                 240
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aga ttt cag agg atc cgc aca ctg aat gct gac ttg atg atg ttt gct   826
Arg Phe Gln Arg Ile Arg Thr Leu Asn Ala Asp Leu Met Met Phe Ala
    245                 250                 255

cac aaa gac cca aga gaa att gac ccc att gtc acc aga aga tat tac   874
His Lys Asp Pro Arg Glu Ile Asp Pro Ile Val Thr Arg Arg Tyr Tyr
260                 265                 270                 275

tac tcg gtc aag gat att tca gtt gga ggg atg tgc atc tgc tat ggt   922
Tyr Ser Val Lys Asp Ile Ser Val Gly Gly Met Cys Ile Cys Tyr Gly
                280                 285                 290

cat gcc agg gct tgt cca ctt gat cca gcg aca aat aaa tct cgc tgt   970
His Ala Arg Ala Cys Pro Leu Asp Pro Ala Thr Asn Lys Ser Arg Cys
            295                 300                 305

gag tgt gag cat aac aca tgt ggc gat agc tgt gat cag tgc tgt cca   1018
Glu Cys Glu His Asn Thr Cys Gly Asp Ser Cys Asp Gln Cys Cys Pro
        310                 315                 320

gga ttc cat cag aaa ccc tgg aga gct gga act ttt cta act aaa act   1066
Gly Phe His Gln Lys Pro Trp Arg Ala Gly Thr Phe Leu Thr Lys Thr
    325                 330                 335

gaa tgt gaa gca tgc aat tgt cat gga aaa gct gaa gaa tgc tat tat   1114
Glu Cys Glu Ala Cys Asn Cys His Gly Lys Ala Glu Glu Cys Tyr Tyr
340                 345                 350                 355

gat gaa aat gtt gcc aga aga aat ctg agt ttg aat ata cgt gga aag   1162
Asp Glu Asn Val Ala Arg Arg Asn Leu Ser Leu Asn Ile Arg Gly Lys
                360                 365                 370

tac att gga ggg ggt gtc tgc att aat tgt acc caa aac act gct ggt   1210
Tyr Ile Gly Gly Gly Val Cys Ile Asn Cys Thr Gln Asn Thr Ala Gly
            375                 380                 385

ata aac tgc gag aca tgt aca gat ggc ttc ttc aga ccc aaa ggg gta   1258
Ile Asn Cys Glu Thr Cys Thr Asp Gly Phe Phe Arg Pro Lys Gly Val
        390                 395                 400

tct cca aat tat cca agg cca tgc cag cca tgt cat tgc gat cca att   1306
Ser Pro Asn Tyr Pro Arg Pro Cys Gln Pro Cys His Cys Asp Pro Ile
    405                 410                 415

ggt tcc tta aat gaa gtc tgt gtc aag gat gag aaa cat gct cga cga   1354
Gly Ser Leu Asn Glu Val Cys Val Lys Asp Glu Lys His Ala Arg Arg
420                 425                 430                 435

ggt ttg gca cct gga tcc tgt cat tgc aaa act ggt ttt gga ggt gtg   1402
Gly Leu Ala Pro Gly Ser Cys His Cys Lys Thr Gly Phe Gly Gly Val
                440                 445                 450

agc tgt gat cgg tgt gcc agg ggc tac act ggc tac ccg gac tgc aaa   1450
Ser Cys Asp Arg Cys Ala Arg Gly Tyr Thr Gly Tyr Pro Asp Cys Lys
            455                 460                 465

gcc tgt aac tgc agt ggg tta ggg agc aaa aat gag gat cct tgt ttt   1498
Ala Cys Asn Cys Ser Gly Leu Gly Ser Lys Asn Glu Asp Pro Cys Phe
        470                 475                 480

ggc ccc tgt atc tgc aag gaa aat gtt gaa gga gga gac tgt agt cgt   1546
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Gly Pro Cys Ile Cys Lys Glu Asn Val Glu Gly Gly Asp Cys Ser Arg
    485                 490                 495

tgc aaa tcc ggc ttc ttc aat ttg caa gag gat aat tgg aaa ggc tgc   1594
Cys Lys Ser Gly Phe Phe Asn Leu Gln Glu Asp Asn Trp Lys Gly Cys
500                 505                 510                 515

gat gag tgt ttc tgt tca ggg gtt tca aac aga tgt cag agt tcc tac   1642
Asp Glu Cys Phe Cys Ser Gly Val Ser Asn Arg Cys Gln Ser Ser Tyr
                520                 525                 530

tgg acc tat ggc aaa ata caa gat atg agt ggc tgg tat ctg act gac   1690
Trp Thr Tyr Gly Lys Ile Gln Asp Met Ser Gly Trp Tyr Leu Thr Asp
            535                 540                 545

ctt cct ggc cgc att cga gtg gct ccc cag cag gac gac ttg gac tca   1738
Leu Pro Gly Arg Ile Arg Val Ala Pro Gln Gln Asp Asp Leu Asp Ser
        550                 555                 560

cct cag cag atc agc atc agt aac gcg gag gcc cgg caa gcc ctg ccg   1786
Pro Gln Gln Ile Ser Ile Ser Asn Ala Glu Ala Arg Gln Ala Leu Pro
    565                 570                 575

cac agc tac tac tgg agc gcg ccg gct ccc tat ctg gga aac aaa ctc   1834
His Ser Tyr Tyr Trp Ser Ala Pro Ala Pro Tyr Leu Gly Asn Lys Leu
580                 585                 590                 595

cca gca gta gga gga cag ttg aca ttt acc ata tca tat gac ctt gaa   1882
Pro Ala Val Gly Gly Gln Leu Thr Phe Thr Ile Ser Tyr Asp Leu Glu
                600                 605                 610

gaa gag gaa gaa gat aca gaa cgt gtt ctc cag ctt atg att atc tta   1930
Glu Glu Glu Glu Asp Thr Glu Arg Val Leu Gln Leu Met Ile Ile Leu
            615                 620                 625

gag ggt aat gac ttg agc atc agc aca gcc caa gat gag gtg tac ctg   1978
Glu Gly Asn Asp Leu Ser Ile Ser Thr Ala Gln Asp Glu Val Tyr Leu
        630                 635                 640

cac cca tct gaa gaa cat act aat gta ttg tta ctt aaa gaa gaa tca   2026
His Pro Ser Glu Glu His Thr Asn Val Leu Leu Leu Lys Glu Glu Ser
    645                 650                 655

ttt acc ata cat ggc aca cat ttt cca gtc cgt aga aag gaa ttt atg   2074
Phe Thr Ile His Gly Thr His Phe Pro Val Arg Arg Lys Glu Phe Met
660                 665                 670                 675

aca gtg ctt gcg aat ttg aag aga gtc ctc cta caa atc aca tac agc   2122
Thr Val Leu Ala Asn Leu Lys Arg Val Leu Leu Gln Ile Thr Tyr Ser
                680                 685                 690

ttt ggg atg gat gcc atc ttc agg ttg agc tct gtt aac ctt gaa tcc   2170
Phe Gly Met Asp Ala Ile Phe Arg Leu Ser Ser Val Asn Leu Glu Ser
            695                 700                 705

gct gtc tcc tat cct act gat gga agc att gca gca gct gta gaa gtg   2218
Ala Val Ser Tyr Pro Thr Asp Gly Ser Ile Ala Ala Ala Val Glu Val
        710                 715                 720

tgt cag tgc cca cca ggg tat act ggc tcc tct tgt gaa tct tgt tgg   2266
Cys Gln Cys Pro Pro Gly Tyr Thr Gly Ser Ser Cys Glu Ser Cys Trp
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    725                 730                 735

cct agg cac agg cga gtt aac ggc act att ttt ggt ggc atc tgt gag   2314
Pro Arg His Arg Arg Val Asn Gly Thr Ile Phe Gly Gly Ile Cys Glu
740                 745                 750                 755

cca tgt cag tgc ttt ggt cat gcg gag tcc tgt gat gac gtc act gga   2362
Pro Cys Gln Cys Phe Gly His Ala Glu Ser Cys Asp Asp Val Thr Gly
                760                 765                 770

gaa tgc ctg aac tgt aag gat cac aca ggt ggc cca tat tgt gat aaa   2410
Glu Cys Leu Asn Cys Lys Asp His Thr Gly Gly Pro Tyr Cys Asp Lys
            775                 780                 785

tgt ctt cct ggt ttc tat ggc gag cct act aaa gga acc tct gaa gac   2458
Cys Leu Pro Gly Phe Tyr Gly Glu Pro Thr Lys Gly Thr Ser Glu Asp
        790                 795                 800

tgt caa ccc tgt gcc tgt cca ctc aat atc cca tcc aat aac ttt agc   2506
Cys Gln Pro Cys Ala Cys Pro Leu Asn Ile Pro Ser Asn Asn Phe Ser
    805                 810                 815

cca acg tgc cat tta gac cgg agt ctt gga ttg atc tgt gat gga tgc   2554
Pro Thr Cys His Leu Asp Arg Ser Leu Gly Leu Ile Cys Asp Gly Cys
820                 825                 830                 835

cct gtc ggg tac aca gga cca cgc tgt gag agg tgt gca gaa ggc tat   2602
Pro Val Gly Tyr Thr Gly Pro Arg Cys Glu Arg Cys Ala Glu Gly Tyr
                840                 845                 850

ttt gga caa ccc tct gta cct gga gga tca tgt cag cca tgc caa tgc   2650
Phe Gly Gln Pro Ser Val Pro Gly Gly Ser Cys Gln Pro Cys Gln Cys
            855                 860                 865

aat gac aac ctt gac ttc tcc atc cct ggc agc tgt gac agc ttg tct   2698
Asn Asp Asn Leu Asp Phe Ser Ile Pro Gly Ser Cys Asp Ser Leu Ser
        870                 875                 880

ggc tcc tgt ctg ata tgt aaa cca ggt aca aca ggc cgg tac tgt gag   2746
Gly Ser Cys Leu Ile Cys Lys Pro Gly Thr Thr Gly Arg Tyr Cys Glu
    885                 890                 895

ctc tgt gct gat gga tat ttt gga gat gca gtt gat gcg aag aac tgt   2794
Leu Cys Ala Asp Gly Tyr Phe Gly Asp Ala Val Asp Ala Lys Asn Cys
900                 905                 910                 915

cag ccc tgt cgc tgt aat gcc ggt ggc tct ttc tct gag gtt tgc cac   2842
Gln Pro Cys Arg Cys Asn Ala Gly Gly Ser Phe Ser Glu Val Cys His
                920                 925                 930

agt caa act gga cag tgt gag tgc aga gcc aac gtt cag ggt cag aga   2890
Ser Gln Thr Gly Gln Cys Glu Cys Arg Ala Asn Val Gln Gly Gln Arg
            935                 940                 945

tgt gac aaa tgc aag gct ggg acc ttt ggc cta caa tca gca agg ggc   2938
Cys Asp Lys Cys Lys Ala Gly Thr Phe Gly Leu Gln Ser Ala Arg Gly
        950                 955                 960

tgt gtt ccc tgc aac tgc aat tct ttt ggg tct aag tca ttc gac tgt   2986
Cys Val Pro Cys Asn Cys Asn Ser Phe Gly Ser Lys Ser Phe Asp Cys
    965                 970                 975
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gaa gag agt gga caa tgt tgg tgc caa cct gga gtc aca ggg aag aaa   3034
Glu Glu Ser Gly Gln Cys Trp Cys Gln Pro Gly Val Thr Gly Lys Lys
980                 985                 990                 995

tgt gac cgc tgt gcc cac ggc tat ttc aac ttc caa gaa gga ggc tgc   3082
Cys Asp Arg Cys Ala His Gly Tyr Phe Asn Phe Gln Glu Gly Gly Cys
                1000                1005                1010

aca gct tgt gaa tgt tct cat ctg ggt aat aat tgt gac cca aag act   3130
Thr Ala Cys Glu Cys Ser His Leu Gly Asn Asn Cys Asp Pro Lys Thr
            1015                1020                1025

ggg cga tgc att tgc cca ccc aat acc att gga gag aaa tgt tct aaa   3178
Gly Arg Cys Ile Cys Pro Pro Asn Thr Ile Gly Glu Lys Cys Ser Lys
        1030                1035                1040

tgt gca ccc aat acc tgg ggc cac agc att acc act ggt tgt aag gct   3226
Cys Ala Pro Asn Thr Trp Gly His Ser Ile Thr Thr Gly Cys Lys Ala
    1045                1050                1055

tgt aac tgc agc aca gtg gga tcc ttg gat ttc caa tgc aat gta aat   3274
Cys Asn Cys Ser Thr Val Gly Ser Leu Asp Phe Gln Cys Asn Val Asn
1060                1065                1070                1075

aca ggc caa tgc aac tgt cat cca aaa ttc tct ggt gca aaa tgt aca   3322
Thr Gly Gln Cys Asn Cys His Pro Lys Phe Ser Gly Ala Lys Cys Thr
                1080                1085                1090

gag tgc agt cga ggt cac tgg aac tac cct cgc tgc aat ctc tgt gac   3370
Glu Cys Ser Arg Gly His Trp Asn Tyr Pro Arg Cys Asn Leu Cys Asp
            1095                1100                1105

tgc ttc ctc cct ggg aca gat gcc aca acc tgt gat tca gag act aaa   3418
Cys Phe Leu Pro Gly Thr Asp Ala Thr Thr Cys Asp Ser Glu Thr Lys
        1110                1115                1120

aaa tgc tcc tgt agt gat caa act ggg cag tgc act tgt aag gtg aat   3466
Lys Cys Ser Cys Ser Asp Gln Thr Gly Gln Cys Thr Cys Lys Val Asn
    1125                1130                1135

gtg gaa ggc atc cac tgt gac aga tgc cgg cct ggc aaa ttc gga ctc   3514
Val Glu Gly Ile His Cys Asp Arg Cys Arg Pro Gly Lys Phe Gly Leu
1140                1145                1150                1155

gat gcc aag aat cca ctt ggc tgc agc agc tgc tat tgc ttc ggc act   3562
Asp Ala Lys Asn Pro Leu Gly Cys Ser Ser Cys Tyr Cys Phe Gly Thr
                1160                1165                1170

act acc cag tgc tct gaa gca aaa gga ctg atc cgg acg tgg gtg act   3610
Thr Thr Gln Cys Ser Glu Ala Lys Gly Leu Ile Arg Thr Trp Val Thr
            1175                1180                1185

ctg aag gct gag cag acc att cta ccc ctg gta gat gag gct ctg cag   3658
Leu Lys Ala Glu Gln Thr Ile Leu Pro Leu Val Asp Glu Ala Leu Gln
        1190                1195                1200

cac acg acc acc aag ggc att gtt ttt caa cat cca gag att gtt gcc   3706
His Thr Thr Thr Lys Gly Ile Val Phe Gln His Pro Glu Ile Val Ala
    1205                1210                1215
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cac atg gac ctg atg aga gaa gat ctc cat ttg gaa cct ttt tat tgg   3754
His Met Asp Leu Met Arg Glu Asp Leu His Leu Glu Pro Phe Tyr Trp
1220               1225                1230                1235

aaa ctt cca gaa caa ttt gaa gga aag aag ttg atg gcc tat ggg ggc   3802
Lys Leu Pro Glu Gln Phe Glu Gly Lys Lys Leu Met Ala Tyr Gly Gly
                1240                1245                1250

aaa ctc aag tat gca atc tat ttc gag gct cgg gaa gaa aca ggt ttc   3850
Lys Leu Lys Tyr Ala Ile Tyr Phe Glu Ala Arg Glu Glu Thr Gly Phe
           1255                1260                1265

tct aca tat aat cct caa gtg atc att cga ggt ggg aca cct act cat   3898
Ser Thr Tyr Asn Pro Gln Val Ile Ile Arg Gly Gly Thr Pro Thr His
       1270                1275                1280

gct aga att atc gtc agg cat atg gct gct cct ctg att ggc caa ttg   3946
Ala Arg Ile Ile Val Arg His Met Ala Ala Pro Leu Ile Gly Gln Leu
   1285                1290                1295

aca agg cat gaa att gaa atg aca gag aaa gaa tgg aaa tat tat ggg   3994
Thr Arg His Glu Ile Glu Met Thr Glu Lys Glu Trp Lys Tyr Tyr Gly
1300               1305                1310                1315

gat gat cct cga gtc cat aga act gtg acc cga gaa gac ttc ttg gat   4042
Asp Asp Pro Arg Val His Arg Thr Val Thr Arg Glu Asp Phe Leu Asp
               1320                1325                1330

ata cta tat gat att cat tac att ctt atc aaa gct act tat gga aat   4090
Ile Leu Tyr Asp Ile His Tyr Ile Leu Ile Lys Ala Thr Tyr Gly Asn
           1335                1340                1345

ttc atg cga caa agc agg att tct gaa atc tca atg gag gta gct gaa   4138
Phe Met Arg Gln Ser Arg Ile Ser Glu Ile Ser Met Glu Val Ala Glu
       1350                1355                1360

caa gga cgt gga aca aca atg act cct cca gct gac ttg att gaa aaa   4186
Gln Gly Arg Gly Thr Thr Met Thr Pro Pro Ala Asp Leu Ile Glu Lys
   1365                1370                1375

tgt gat tgt ccc ctg ggc tat tct ggc ctg tcc tgt gag gca tgc ttg   4234
Cys Asp Cys Pro Leu Gly Tyr Ser Gly Leu Ser Cys Glu Ala Cys Leu
1380               1385                1390                1395

ccg gga ttt tat cga ctg cgt tct caa cca ggt ggc cgc acc cct gga   4282
Pro Gly Phe Tyr Arg Leu Arg Ser Gln Pro Gly Gly Arg Thr Pro Gly
               1400                1405                1410

cca acc ctg ggc acc tgt gtt cca tgt caa tgt aat gga cac agc agc   4330
Pro Thr Leu Gly Thr Cys Val Pro Cys Gln Cys Asn Gly His Ser Ser
           1415                1420                1425

ctg tgt gac cct gaa aca tcg ata tgc cag aat tgt caa cat cac act   4378
Leu Cys Asp Pro Glu Thr Ser Ile Cys Gln Asn Cys Gln His His Thr
       1430                1435                1440

gct ggt gac ttc tgt gaa cga tgt gct ctt gga tac tat gga att gtc   4426
Ala Gly Asp Phe Cys Glu Arg Cys Ala Leu Gly Tyr Tyr Gly Ile Val
   1445                1450                1455

aag gga ttg cca aat gac tgt cag caa tgt gcc tgc cct ctg att tct   4474
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Lys Gly Leu Pro Asn Asp Cys Gln Gln Cys Ala Cys Pro Leu Ile Ser
1460                1465                1470                1475

tcc agt aac aat ttc agc ccc tct tgt gtc gca gaa gga ctt gac gac   4522
Ser Ser Asn Asn Phe Ser Pro Ser Cys Val Ala Glu Gly Leu Asp Asp
                1480                1485                1490

tac cgc tgc acg gct tgt cca cgg gga tat gaa ggc cag tac tgt gaa   4570
Tyr Arg Cys Thr Ala Cys Pro Arg Gly Tyr Glu Gly Gln Tyr Cys Glu
            1495                1500                1505

agg tgt gcc cct ggc tat act ggc agt cca ggc aac cct gga ggc tcc   4618
Arg Cys Ala Pro Gly Tyr Thr Gly Ser Pro Gly Asn Pro Gly Gly Ser
        1510                1515                1520

tgc caa gaa tgt gag tgt gat ccc tat ggc tca ctg cct gtg ccc tgt   4666
Cys Gln Glu Cys Glu Cys Asp Pro Tyr Gly Ser Leu Pro Val Pro Cys
    1525                1530                1535

gac cct gtc aca gga ttc tgc acg tgc cga cct gga gcc acg gga agg   4714
Asp Pro Val Thr Gly Phe Cys Thr Cys Arg Pro Gly Ala Thr Gly Arg
1540                1545                1550                1555

aag tgt gac ggc tgc aag cac tgg cat gca cgc gag ggc tgg gag tgt   4762
Lys Cys Asp Gly Cys Lys His Trp His Ala Arg Glu Gly Trp Glu Cys
                1560                1565                1570

gtt ttt tgt gga gat gag tgc act ggc ctt ctt ctc ggt gac ttg gct   4810
Val Phe Cys Gly Asp Glu Cys Thr Gly Leu Leu Leu Gly Asp Leu Ala
            1575                1580                1585

cgc ctg gag cag atg gtc atg agc atc aac ctc act ggt ccg ctg cct   4858
Arg Leu Glu Gln Met Val Met Ser Ile Asn Leu Thr Gly Pro Leu Pro
        1590                1595                1600

gcg cca tat aaa atg ctg tat ggt ctt gaa aat atg act cag gag cta   4906
Ala Pro Tyr Lys Met Leu Tyr Gly Leu Glu Asn Met Thr Gln Glu Leu
    1605                1610                1615

aag cac ttg ctg tca cct cag cgg gcc cca gag agg ctt att cag ctg   4954
Lys His Leu Leu Ser Pro Gln Arg Ala Pro Glu Arg Leu Ile Gln Leu
1620                1625                1630                1635

gca gag ggc aat ctg aat aca ctc gtg acc gaa atg aac gag ctg ctg   5002
Ala Glu Gly Asn Leu Asn Thr Leu Val Thr Glu Met Asn Glu Leu Leu
                1640                1645                1650

acc agg gct acc aaa gtg aca gca gat ggc gag cag acc gga cag gat   5050
Thr Arg Ala Thr Lys Val Thr Ala Asp Gly Glu Gln Thr Gly Gln Asp
            1655                1660                1665

gct gag agg acc aac aca aga gca aag tcc ctg gga gaa ttc att aag   5098
Ala Glu Arg Thr Asn Thr Arg Ala Lys Ser Leu Gly Glu Phe Ile Lys
        1670                1675                1680

gag ctt gcc cgg gat gca gaa gct gta aat gaa aaa gct ata aaa cta   5146
Glu Leu Ala Arg Asp Ala Glu Ala Val Asn Glu Lys Ala Ile Lys Leu
    1685                1690                1695

aat gaa act cta gga act cga gac gag gcc ttt gag aga aat ttg gaa   5194
Asn Glu Thr Leu Gly Thr Arg Asp Glu Ala Phe Glu Arg Asn Leu Glu
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1700                1705                1710                1715

ggg ctt cag aaa gag att gac cag atg att aaa gaa ctg agg agg aaa   5242
Gly Leu Gln Lys Glu Ile Asp Gln Met Ile Lys Glu Leu Arg Arg Lys
                1720                1725                1730

aat cta gag aca caa aag gaa att gct gaa gat gag ttg gta gct gca   5290
Asn Leu Glu Thr Gln Lys Glu Ile Ala Glu Asp Glu Leu Val Ala Ala
            1735                1740                1745

gaa gcc ctt ctg aaa aaa gtg aag aag ctg ttt gga gag tcc cgg ggg   5338
Glu Ala Leu Leu Lys Lys Val Lys Lys Leu Phe Gly Glu Ser Arg Gly
        1750                1755                1760

gaa aat gaa gaa atg gag aag gat ctc cgg gaa aaa ctg gct gac tac   5386
Glu Asn Glu Glu Met Glu Lys Asp Leu Arg Glu Lys Leu Ala Asp Tyr
    1765                1770                1775

aaa aac aaa gtt gat gat gct tgg gac ctt ttg aga gaa gcc aca gat   5434
Lys Asn Lys Val Asp Asp Ala Trp Asp Leu Leu Arg Glu Ala Thr Asp
1780                1785                1790                1795

aaa atc aga gaa gct aat cgc cta ttt gca gta aat cag aaa aac atg   5482
Lys Ile Arg Glu Ala Asn Arg Leu Phe Ala Val Asn Gln Lys Asn Met
                1800                1805                1810

act gca ttg gag aaa aag aag gag gct gtt gag agc ggc aaa cga caa   5530
Thr Ala Leu Glu Lys Lys Lys Glu Ala Val Glu Ser Gly Lys Arg Gln
            1815                1820                1825

att gag aac act tta aaa gaa ggc aat gac ata ctc gat gaa gcc aac   5578
Ile Glu Asn Thr Leu Lys Glu Gly Asn Asp Ile Leu Asp Glu Ala Asn
        1830                1835                1840

cgt ctt gca gat gaa atc aac tcc atc ata gac tat gtt gaa gac atc   5626
Arg Leu Ala Asp Glu Ile Asn Ser Ile Ile Asp Tyr Val Glu Asp Ile
    1845                1850                1855

caa act aaa ttg cca cct atg tct gag gag ctt aat gat aaa ata gat   5674
Gln Thr Lys Leu Pro Pro Met Ser Glu Glu Leu Asn Asp Lys Ile Asp
1860                1865                1870                1875

gac ctc tcc caa gaa ata aag gac agg aag ctt gct gag aag gtg tcc   5722
Asp Leu Ser Gln Glu Ile Lys Asp Arg Lys Leu Ala Glu Lys Val Ser
                1880                1885                1890

cag gct gag agc cac gca gct cag ttg aat gac tca tct gct gtc ctt   5770
Gln Ala Glu Ser His Ala Ala Gln Leu Asn Asp Ser Ser Ala Val Leu
            1895                1900                1905

gat gga atc ctt gat gag gct aaa aac atc tcc ttc aat gcc act gca   5818
Asp Gly Ile Leu Asp Glu Ala Lys Asn Ile Ser Phe Asn Ala Thr Ala
        1910                1915                1920

gcc ttc aaa gct tac agc aat att aag gac tat att gat gaa gct gag   5866
Ala Phe Lys Ala Tyr Ser Asn Ile Lys Asp Tyr Ile Asp Glu Ala Glu
    1925                1930                1935

aaa gtt gcc aaa gaa gcc aaa gat ctt gca cat gaa gct aca aaa ctg   5914
Lys Val Ala Lys Glu Ala Lys Asp Leu Ala His Glu Ala Thr Lys Leu
1940                1945                1950                1955
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gca aca ggt cct cgg ggt tta tta aag gaa gat gcc aaa ggc tgt ctt   5962
Ala Thr Gly Pro Arg Gly Leu Leu Lys Glu Asp Ala Lys Gly Cys Leu
                1960                1965                1970

cag aaa agc ttc agg att ctt aac gaa gcc aag aag tta gca aat gat   6010
Gln Lys Ser Phe Arg Ile Leu Asn Glu Ala Lys Lys Leu Ala Asn Asp
            1975                1980                1985

gta aaa gaa aat gaa gac cat cta aat ggc tta aaa acc agg ata gaa   6058
Val Lys Glu Asn Glu Asp His Leu Asn Gly Leu Lys Thr Arg Ile Glu
        1990                1995                2000

aat gct gat gct aga aat ggg gat ctc ttg aga act ttg aat gac act   6106
Asn Ala Asp Ala Arg Asn Gly Asp Leu Leu Arg Thr Leu Asn Asp Thr
    2005                2010                2015

ttg gga aag tta tca gct att cca aat gat aca gct gct aaa ctg caa   6154
Leu Gly Lys Leu Ser Ala Ile Pro Asn Asp Thr Ala Ala Lys Leu Gln
2020                2025                2030                2035

gct gtt aag gac aaa gcc aga caa gcc aac gac aca gct aaa gat gta   6202
Ala Val Lys Asp Lys Ala Arg Gln Ala Asn Asp Thr Ala Lys Asp Val
                2040                2045                2050

ctg gca cag att aca gag ctc cac cag aac ctc gat ggc ctg aag aag   6250
Leu Ala Gln Ile Thr Glu Leu His Gln Asn Leu Asp Gly Leu Lys Lys
            2055                2060                2065

aat tac aat aaa cta gca gac agc gtc gcc aaa acg aat gct gtg gtt   6298
Asn Tyr Asn Lys Leu Ala Asp Ser Val Ala Lys Thr Asn Ala Val Val
        2070                2075                2080

aaa gat cct tcc aag aac aaa atc att gcc gat gca gat gcc act gtc   6346
Lys Asp Pro Ser Lys Asn Lys Ile Ile Ala Asp Ala Asp Ala Thr Val
    2085                2090                2095

aaa aat tta gaa cag gaa gct gac cgg cta ata gat aaa ctc aaa ccc   6394
Lys Asn Leu Glu Gln Glu Ala Asp Arg Leu Ile Asp Lys Leu Lys Pro
2100                2105                2110                2115

atc aag gaa ctt gag gat aac cta aag aaa aac atc tct gag ata aag   6442
Ile Lys Glu Leu Glu Asp Asn Leu Lys Lys Asn Ile Ser Glu Ile Lys
                2120                2125                2130

gaa ttg ata aac caa gct cgg aaa caa gcc aat tct atc aaa gta tct   6490
Glu Leu Ile Asn Gln Ala Arg Lys Gln Ala Asn Ser Ile Lys Val Ser
            2135                2140                2145

gtg tct tca gga ggt gac tgc att cga aca tac aaa cca gaa atc aag   6538
Val Ser Ser Gly Gly Asp Cys Ile Arg Thr Tyr Lys Pro Glu Ile Lys
        2150                2155                2160

aaa gga agt tac aat aat att gtt gtc aac gta aag aca gct gtt gct   6586
Lys Gly Ser Tyr Asn Asn Ile Val Val Asn Val Lys Thr Ala Val Ala
    2165                2170                2175

gat aac ctc ctc ttt tat ctt gga agt gcc aaa ttt att gac ttt ctg   6634
Asp Asn Leu Leu Phe Tyr Leu Gly Ser Ala Lys Phe Ile Asp Phe Leu
2180                2185                2190                2195
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gct ata gaa atg cgt aaa ggc aaa gtc agc ttc ctc tgg gat gtt gga   6682
Ala Ile Glu Met Arg Lys Gly Lys Val Ser Phe Leu Trp Asp Val Gly
             2200                2205                2210

tct gga gtt gga cgt gta gag tac cca gat ttg act att gat gac tca   6730
Ser Gly Val Gly Arg Val Glu Tyr Pro Asp Leu Thr Ile Asp Asp Ser
          2215                2220                2225

tat tgg tac cgt atc gta gca tca aga act ggg aga aat gga act att   6778
Tyr Trp Tyr Arg Ile Val Ala Ser Arg Thr Gly Arg Asn Gly Thr Ile
       2230                2235                2240

tct gtg aga gcc ctg gat gga ccc aaa gcc agc att gtg ccc agc aca   6826
Ser Val Arg Ala Leu Asp Gly Pro Lys Ala Ser Ile Val Pro Ser Thr
   2245                2250                2255

cac cat tcg acg tct cct cca ggg tac acg att cta gat gtg gat gca   6874
His His Ser Thr Ser Pro Pro Gly Tyr Thr Ile Leu Asp Val Asp Ala
2260                2265                2270                2275

aat gca atg ctg ttt gtt ggt ggc ctg act ggg aaa tta aag aag gct   6922
Asn Ala Met Leu Phe Val Gly Gly Leu Thr Gly Lys Leu Lys Lys Ala
             2280                2285                2290

gat gct gta cgt gtg att aca ttc act ggc tgc atg gga gaa aca tac   6970
Asp Ala Val Arg Val Ile Thr Phe Thr Gly Cys Met Gly Glu Thr Tyr
          2295                2300                2305

ttt gac aac aaa cct ata ggt ttg tgg aat ttc cga gaa aaa gaa ggt   7018
Phe Asp Asn Lys Pro Ile Gly Leu Trp Asn Phe Arg Glu Lys Glu Gly
       2310                2315                2320

gac tgc aaa gga tgc act gtc agt cct cag gtg gaa gat agt gag ggg   7066
Asp Cys Lys Gly Cys Thr Val Ser Pro Gln Val Glu Asp Ser Glu Gly
   2325                2330                2335

act att caa ttt gat gga gaa ggt tat gca ttg gtc agc cgt ccc att   7114
Thr Ile Gln Phe Asp Gly Glu Gly Tyr Ala Leu Val Ser Arg Pro Ile
2340                2345                2350                2355

cgc tgg tac ccc aac atc tcc act gtc atg ttc aag ttc aga aca ttt   7162
Arg Trp Tyr Pro Asn Ile Ser Thr Val Met Phe Lys Phe Arg Thr Phe
             2360                2365                2370

tct tcg agt gct ctt ctg atg tat ctt gcc aca cga gac ctg aga gat   7210
Ser Ser Ser Ala Leu Leu Met Tyr Leu Ala Thr Arg Asp Leu Arg Asp
          2375                2380                2385

ttc atg agt gtg gag ctc act gat ggg cac ata aaa gtc agt tac gat   7258
Phe Met Ser Val Glu Leu Thr Asp Gly His Ile Lys Val Ser Tyr Asp
       2390                2395                2400

ctg ggc tca gga atg gct tcc gtt gtc agc aat caa aac cat aat gat   7306
Leu Gly Ser Gly Met Ala Ser Val Val Ser Asn Gln Asn His Asn Asp
   2405                2410                2415

ggg aaa tgg aaa tca ttc act ctg tca aga att caa aaa caa gcc aat   7354
Gly Lys Trp Lys Ser Phe Thr Leu Ser Arg Ile Gln Lys Gln Ala Asn
2420                2425                2430                2435

ata tca att gta gat ata gat act aat cag gag gag aat ata gca act   7402
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Ile Ser Ile Val Asp Ile Asp Thr Asn Gln Glu Glu Asn Ile Ala Thr
                2440                2445                2450

tcg tct tct gga aac aac ttt ggt ctt gac ttg aaa gca gat gac aaa   7450
Ser Ser Ser Gly Asn Asn Phe Gly Leu Asp Leu Lys Ala Asp Asp Lys
            2455                2460                2465

ata tat ttt ggt ggc ctg cca acg ctg aga aac ttg agt atg aaa gca   7498
Ile Tyr Phe Gly Gly Leu Pro Thr Leu Arg Asn Leu Ser Met Lys Ala
        2470                2475                2480

agg cca gaa gta aat ctg aag aaa tat tcc ggc tgc ctc aaa gat att   7546
Arg Pro Glu Val Asn Leu Lys Lys Tyr Ser Gly Cys Leu Lys Asp Ile
    2485                2490                2495

gaa att tca aga act ccg tac aat ata ctc agt agt ccc gat tat gtt   7594
Glu Ile Ser Arg Thr Pro Tyr Asn Ile Leu Ser Ser Pro Asp Tyr Val
2500                2505                2510                2515

ggt gtt acc aaa gga tgt tcc ctg gag aat gtt tac aca gtt agc ttt   7642
Gly Val Thr Lys Gly Cys Ser Leu Glu Asn Val Tyr Thr Val Ser Phe
                2520                2525                2530

cct aag cct ggt ttt gtg gag ctc tcc cct gtg cca att gat gta gga   7690
Pro Lys Pro Gly Phe Val Glu Leu Ser Pro Val Pro Ile Asp Val Gly
            2535                2540                2545

aca gaa atc aac ctg tca ttc agc acc aag aat gag tcc ggc atc att   7738
Thr Glu Ile Asn Leu Ser Phe Ser Thr Lys Asn Glu Ser Gly Ile Ile
        2550                2555                2560

ctt ttg gga agt gga ggg aca cca gca cca cct agg aga aaa cga agg   7786
Leu Leu Gly Ser Gly Gly Thr Pro Ala Pro Pro Arg Arg Lys Arg Arg
    2565                2570                2575

cag act gga cag gcc tat tat gta ata ctc ctc aac agg ggc cgt ctg   7834
Gln Thr Gly Gln Ala Tyr Tyr Val Ile Leu Leu Asn Arg Gly Arg Leu
2580                2585                2590                2595

gaa gtg cat ctc tcc aca ggg gca cga aca atg agg aaa att gtc atc   7882
Glu Val His Leu Ser Thr Gly Ala Arg Thr Met Arg Lys Ile Val Ile
                2600                2605                2610

aga cca gag ccg aat ctg ttt cat gat gga aga gaa cat tcc gtt cat   7930
Arg Pro Glu Pro Asn Leu Phe His Asp Gly Arg Glu His Ser Val His
            2615                2620                2625

gta gag cga act aga ggc atc ttt aca gtt caa gtg gat gaa aac aga   7978
Val Glu Arg Thr Arg Gly Ile Phe Thr Val Gln Val Asp Glu Asn Arg
        2630                2635                2640

aga tac atg caa aac ctg aca gtt gaa cag cct atc gaa gtt aaa aag   8026
Arg Tyr Met Gln Asn Leu Thr Val Glu Gln Pro Ile Glu Val Lys Lys
    2645                2650                2655

ctt ttc gtt ggg ggt gct cca cct gaa ttt caa cct tcc cca ctc aga   8074
Leu Phe Val Gly Gly Ala Pro Pro Glu Phe Gln Pro Ser Pro Leu Arg
2660                2665                2670                2675

aat att cct cct ttt gaa ggc tgc ata tgg aat ctt gtt att aac tct   8122
Asn Ile Pro Pro Phe Glu Gly Cys Ile Trp Asn Leu Val Ile Asn Ser
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                2680                2685                2690

gtc ccc atg gac ttt gca agg cct gtg tcc ttc aaa aat gct gac att   8170
Val Pro Met Asp Phe Ala Arg Pro Val Ser Phe Lys Asn Ala Asp Ile
          2695                2700                2705

ggt cgc tgt gcc cat cag aaa ctc cgt gaa gat gaa gat gga gca gct   8218
Gly Arg Cys Ala His Gln Lys Leu Arg Glu Asp Glu Asp Gly Ala Ala
       2710                2715                2720

cca gct gaa ata gtt atc cag cct gag cca gtt ccc acc cca gcc ttt   8266
Pro Ala Glu Ile Val Ile Gln Pro Glu Pro Val Pro Thr Pro Ala Phe
   2725                2730                2735

cct acg ccc acc cca gtt ctg aca cat ggt cct tgt gct gca gaa tca   8314
Pro Thr Pro Thr Pro Val Leu Thr His Gly Pro Cys Ala Ala Glu Ser
2740                2745                2750                2755

gaa cca gct ctt ttg ata ggg agc aag cag ttc ggg ctt tca aga aac   8362
Glu Pro Ala Leu Leu Ile Gly Ser Lys Gln Phe Gly Leu Ser Arg Asn
               2760                2765                2770

agt cac att gca att gca ttt gat gac acc aaa gtt aaa aac cgt ctc   8410
Ser His Ile Ala Ile Ala Phe Asp Asp Thr Lys Val Lys Asn Arg Leu
          2775                2780                2785

aca att gag ttg gaa gta aga acc gaa gct gaa tcc ggc ttg ctt ttt   8458
Thr Ile Glu Leu Glu Val Arg Thr Glu Ala Glu Ser Gly Leu Leu Phe
       2790                2795                2800

tac atg gct gcg atc aat cat gct gat ttt gca aca gtt cag ctg aga   8506
Tyr Met Ala Ala Ile Asn His Ala Asp Phe Ala Thr Val Gln Leu Arg
   2805                2810                2815

aat gga ttg ccc tac ttc agc tat gac ttg ggg agt ggg gac acc cac   8554
Asn Gly Leu Pro Tyr Phe Ser Tyr Asp Leu Gly Ser Gly Asp Thr His
2820                2825                2830                2835

acc atg atc ccc acc aaa atc aat gat ggc cag tgg cac aag att aag   8602
Thr Met Ile Pro Thr Lys Ile Asn Asp Gly Gln Trp His Lys Ile Lys
               2840                2845                2850

ata atg aga agt aag caa gaa gga att ctt tat gta gat ggg gct tcc   8650
Ile Met Arg Ser Lys Gln Glu Gly Ile Leu Tyr Val Asp Gly Ala Ser
          2855                2860                2865

aac aga acc atc agt ccc aaa aaa gcc gac atc ctg gat gtc gtg gga   8698
Asn Arg Thr Ile Ser Pro Lys Lys Ala Asp Ile Leu Asp Val Val Gly
       2870                2875                2880

atg ctg tat gtt ggt ggg tta ccc atc aac tac act acc cga aga att   8746
Met Leu Tyr Val Gly Gly Leu Pro Ile Asn Tyr Thr Thr Arg Arg Ile
   2885                2890                2895

ggt cca gtg acc tat agc att gat ggc tgc gtc agg aat ctc cac atg   8794
Gly Pro Val Thr Tyr Ser Ile Asp Gly Cys Val Arg Asn Leu His Met
2900                2905                2910                2915

gca gag gcc cct gcc gat ctg gaa caa ccc acc tcc agc ttc cat gtt   8842
Ala Glu Ala Pro Ala Asp Leu Glu Gln Pro Thr Ser Ser Phe His Val
               2920                2925                2930
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ggg aca tgt ttt gca aat gct cag agg gga aca tat ttt gac gga acc   8890
Gly Thr Cys Phe Ala Asn Ala Gln Arg Gly Thr Tyr Phe Asp Gly Thr
          2935                2940                2945

ggt ttt gcc aaa gca gtt ggt gga ttc aaa gtg gga ttg gac ctt ctt   8938
Gly Phe Ala Lys Ala Val Gly Gly Phe Lys Val Gly Leu Asp Leu Leu
       2950                2955                2960

gta gaa ttt gaa ttc gcg aca act aca acg act gga gtt ctt ctg ggg   8986
Val Glu Phe Glu Phe Ala Thr Thr Thr Thr Thr Gly Val Leu Leu Gly
   2965                2970                2975

atc agt agt caa aaa atg gat gga atg ggt att gaa atg att gat gaa   9034
Ile Ser Ser Gln Lys Met Asp Gly Met Gly Ile Glu Met Ile Asp Glu
2980                2985                2990                2995

aag ttg atg ttt cat gtg gac aat ggt gcg ggc aga ttc act gct gtc   9082
Lys Leu Met Phe His Val Asp Asn Gly Ala Gly Arg Phe Thr Ala Val
               3000                3005                3010

tat gat gct ggg gtt cca ggg cat ttg tgt gat gga caa tgg cat aaa   9130
Tyr Asp Ala Gly Val Pro Gly His Leu Cys Asp Gly Gln Trp His Lys
          3015                3020                3025

gtc act gcc aac aag atc aaa cac cgc att gag ctc aca gtc gat ggg   9178
Val Thr Ala Asn Lys Ile Lys His Arg Ile Glu Leu Thr Val Asp Gly
       3030                3035                3040

aac cag gtg gaa gcc caa agc cca aac cca gca tct aca tca gct gac   9226
Asn Gln Val Glu Ala Gln Ser Pro Asn Pro Ala Ser Thr Ser Ala Asp
   3045                3050                3055

aca aat gac cct gtg ttt gtt gga ggc ttc cca gat gac ctc aag cag   9274
Thr Asn Asp Pro Val Phe Val Gly Gly Phe Pro Asp Asp Leu Lys Gln
3060                3065                3070                3075

ttt ggc cta aca acc agt att ccg ttc cga ggt tgc atc aga tcc ctg   9322
Phe Gly Leu Thr Thr Ser Ile Pro Phe Arg Gly Cys Ile Arg Ser Leu
               3080                3085                3090

aag ctc acc aaa ggc aca gca agc cac tgg agg tta att ttg cca agg   9370
Lys Leu Thr Lys Gly Thr Ala Ser His Trp Arg Leu Ile Leu Pro Arg
          3095                3100                3105

ccc tgg aac tgaggggcgt tcaacctgta tcatgcccag ccaactaata          9419
Pro Trp Asn
       3110

aaaataagtg taaccccagg aagagtctgt caaaacaagt atatcaagta aaacaaacaa 9479

atatatttta cctatatatg ttaattaaac taatttgtgc atgtacatag aattc      9534


<210> 6
<211> 3110
<212> PRT
<213> Homo sapiens

<400> 6
Met Pro Gly Ala Ala Gly Val Leu Leu Leu Leu Leu Leu Ser Gly Gly
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 1               5                  10                  15

Leu Gly Gly Val Gln Ala Gln Arg Pro Gln Gln Gln Arg Gln Ser Gln
            20                  25                  30

Ala His Gln Gln Arg Gly Leu Phe Pro Ala Val Leu Asn Leu Ala Ser
        35                  40                  45

Asn Ala Leu Ile Thr Thr Asn Ala Thr Cys Gly Glu Lys Gly Pro Glu
    50                  55                  60

Met Tyr Cys Lys Leu Val Glu His Val Pro Gly Gln Pro Val Arg Asn
65                  70                  75                  80

Pro Gln Cys Arg Ile Cys Asn Gln Asn Ser Ser Asn Pro Asn Gln Arg
                85                  90                  95

His Pro Ile Thr Asn Ala Ile Asp Gly Lys Asn Thr Trp Trp Gln Ser
            100                 105                 110

Pro Ser Ile Lys Asn Gly Ile Glu Tyr His Tyr Val Thr Ile Thr Leu
        115                 120                 125

Asp Leu Gln Gln Val Phe Gln Ile Ala Tyr Val Ile Val Lys Ala Ala
    130                 135                 140

Asn Ser Pro Arg Pro Gly Asn Trp Ile Leu Glu Arg Ser Leu Asp Asp
145                 150                 155                 160

Val Glu Tyr Lys Pro Trp Gln Tyr His Ala Val Thr Asp Thr Glu Cys
                165                 170                 175

Leu Thr Leu Tyr Asn Ile Tyr Pro Arg Thr Gly Pro Pro Ser Tyr Ala
            180                 185                 190

Lys Asp Asp Glu Val Ile Cys Thr Ser Phe Tyr Ser Lys Ile His Pro
        195                 200                 205

Leu Glu Asn Gly Glu Ile His Ile Ser Leu Ile Asn Gly Arg Pro Ser
    210                 215                 220

Ala Asp Asp Pro Ser Pro Glu Leu Leu Glu Phe Thr Ser Ala Arg Tyr
225                 230                 235                 240

Ile Arg Leu Arg Phe Gln Arg Ile Arg Thr Leu Asn Ala Asp Leu Met
                245                 250                 255

Met Phe Ala His Lys Asp Pro Arg Glu Ile Asp Pro Ile Val Thr Arg
            260                 265                 270

Arg Tyr Tyr Tyr Ser Val Lys Asp Ile Ser Val Gly Gly Met Cys Ile
        275                 280                 285

Cys Tyr Gly His Ala Arg Ala Cys Pro Leu Asp Pro Ala Thr Asn Lys
    290                 295                 300

Ser Arg Cys Glu Cys Glu His Asn Thr Cys Gly Asp Ser Cys Asp Gln
305                 310                 315                 320

Cys Cys Pro Gly Phe His Gln Lys Pro Trp Arg Ala Gly Thr Phe Leu
                325                 330                 335
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Thr Lys Thr Glu Cys Glu Ala Cys Asn Cys His Gly Lys Ala Glu Glu
            340                 345                 350

Cys Tyr Tyr Asp Glu Asn Val Ala Arg Arg Asn Leu Ser Leu Asn Ile
        355                 360                 365

Arg Gly Lys Tyr Ile Gly Gly Gly Val Cys Ile Asn Cys Thr Gln Asn
    370                 375                 380

Thr Ala Gly Ile Asn Cys Glu Thr Cys Thr Asp Gly Phe Phe Arg Pro
385                 390                 395                 400

Lys Gly Val Ser Pro Asn Tyr Pro Arg Pro Cys Gln Pro Cys His Cys
                405                 410                 415

Asp Pro Ile Gly Ser Leu Asn Glu Val Cys Val Lys Asp Glu Lys His
            420                 425                 430

Ala Arg Arg Gly Leu Ala Pro Gly Ser Cys His Cys Lys Thr Gly Phe
        435                 440                 445

Gly Gly Val Ser Cys Asp Arg Cys Ala Arg Gly Tyr Thr Gly Tyr Pro
    450                 455                 460

Asp Cys Lys Ala Cys Asn Cys Ser Gly Leu Gly Ser Lys Asn Glu Asp
465                 470                 475                 480

Pro Cys Phe Gly Pro Cys Ile Cys Lys Glu Asn Val Glu Gly Gly Asp
                485                 490                 495

Cys Ser Arg Cys Lys Ser Gly Phe Phe Asn Leu Gln Glu Asp Asn Trp
            500                 505                 510

Lys Gly Cys Asp Glu Cys Phe Cys Ser Gly Val Ser Asn Arg Cys Gln
        515                 520                 525

Ser Ser Tyr Trp Thr Tyr Gly Lys Ile Gln Asp Met Ser Gly Trp Tyr
    530                 535                 540

Leu Thr Asp Leu Pro Gly Arg Ile Arg Val Ala Pro Gln Gln Asp Asp
545                 550                 555                 560

Leu Asp Ser Pro Gln Gln Ile Ser Ile Ser Asn Ala Glu Ala Arg Gln
                565                 570                 575

Ala Leu Pro His Ser Tyr Tyr Trp Ser Ala Pro Ala Pro Tyr Leu Gly
            580                 585                 590

Asn Lys Leu Pro Ala Val Gly Gly Gln Leu Thr Phe Thr Ile Ser Tyr
        595                 600                 605

Asp Leu Glu Glu Glu Glu Glu Asp Thr Glu Arg Val Leu Gln Leu Met
    610                 615                 620

Ile Ile Leu Glu Gly Asn Asp Leu Ser Ile Ser Thr Ala Gln Asp Glu
625                 630                 635                 640

Val Tyr Leu His Pro Ser Glu Glu His Thr Asn Val Leu Leu Leu Lys
                645                 650                 655
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Glu Glu Ser Phe Thr Ile His Gly Thr His Phe Pro Val Arg Arg Lys
            660                 665                 670

Glu Phe Met Thr Val Leu Ala Asn Leu Lys Arg Val Leu Leu Gln Ile
        675                 680                 685

Thr Tyr Ser Phe Gly Met Asp Ala Ile Phe Arg Leu Ser Ser Val Asn
    690                 695                 700

Leu Glu Ser Ala Val Ser Tyr Pro Thr Asp Gly Ser Ile Ala Ala Ala
705                 710                 715                 720

Val Glu Val Cys Gln Cys Pro Pro Gly Tyr Thr Gly Ser Ser Cys Glu
                725                 730                 735

Ser Cys Trp Pro Arg His Arg Arg Val Asn Gly Thr Ile Phe Gly Gly
            740                 745                 750

Ile Cys Glu Pro Cys Gln Cys Phe Gly His Ala Glu Ser Cys Asp Asp
        755                 760                 765

Val Thr Gly Glu Cys Leu Asn Cys Lys Asp His Thr Gly Gly Pro Tyr
    770                 775                 780

Cys Asp Lys Cys Leu Pro Gly Phe Tyr Gly Glu Pro Thr Lys Gly Thr
785                 790                 795                 800

Ser Glu Asp Cys Gln Pro Cys Ala Cys Pro Leu Asn Ile Pro Ser Asn
                805                 810                 815

Asn Phe Ser Pro Thr Cys His Leu Asp Arg Ser Leu Gly Leu Ile Cys
            820                 825                 830

Asp Gly Cys Pro Val Gly Tyr Thr Gly Pro Arg Cys Glu Arg Cys Ala
        835                 840                 845

Glu Gly Tyr Phe Gly Gln Pro Ser Val Pro Gly Gly Ser Cys Gln Pro
    850                 855                 860

Cys Gln Cys Asn Asp Asn Leu Asp Phe Ser Ile Pro Gly Ser Cys Asp
865                 870                 875                 880

Ser Leu Ser Gly Ser Cys Leu Ile Cys Lys Pro Gly Thr Thr Gly Arg
                885                 890                 895

Tyr Cys Glu Leu Cys Ala Asp Gly Tyr Phe Gly Asp Ala Val Asp Ala
            900                 905                 910

Lys Asn Cys Gln Pro Cys Arg Cys Asn Ala Gly Gly Ser Phe Ser Glu
        915                 920                 925

Val Cys His Ser Gln Thr Gly Gln Cys Glu Cys Arg Ala Asn Val Gln
    930                 935                 940

Gly Gln Arg Cys Asp Lys Cys Lys Ala Gly Thr Phe Gly Leu Gln Ser
945                 950                 955                 960

Ala Arg Gly Cys Val Pro Cys Asn Cys Asn Ser Phe Gly Ser Lys Ser
                965                 970                 975

Phe Asp Cys Glu Glu Ser Gly Gln Cys Trp Cys Gln Pro Gly Val Thr
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            980                 985                 990

Gly Lys Lys Cys Asp Arg Cys Ala His Gly Tyr Phe Asn Phe Gln Glu
        995                1000                1005

Gly Gly Cys Thr Ala Cys Glu Cys Ser His Leu Gly Asn Asn Cys Asp
   1010                1015                1020

Pro Lys Thr Gly Arg Cys Ile Cys Pro Pro Asn Thr Ile Gly Glu Lys
025                1030                1035                1040

Cys Ser Lys Cys Ala Pro Asn Thr Trp Gly His Ser Ile Thr Thr Gly
               1045                1050                1055

Cys Lys Ala Cys Asn Cys Ser Thr Val Gly Ser Leu Asp Phe Gln Cys
            1060                1065                1070

Asn Val Asn Thr Gly Gln Cys Asn Cys His Pro Lys Phe Ser Gly Ala
       1075                1080                1085

Lys Cys Thr Glu Cys Ser Arg Gly His Trp Asn Tyr Pro Arg Cys Asn
   1090                1095                1100

Leu Cys Asp Cys Phe Leu Pro Gly Thr Asp Ala Thr Thr Cys Asp Ser
105                1110                1115                1120

Glu Thr Lys Lys Cys Ser Cys Ser Asp Gln Thr Gly Gln Cys Thr Cys
               1125                1130                1135

Lys Val Asn Val Glu Gly Ile His Cys Asp Arg Cys Arg Pro Gly Lys
            1140                1145                1150

Phe Gly Leu Asp Ala Lys Asn Pro Leu Gly Cys Ser Ser Cys Tyr Cys
       1155                1160                1165

Phe Gly Thr Thr Thr Gln Cys Ser Glu Ala Lys Gly Leu Ile Arg Thr
   1170                1175                1180

Trp Val Thr Leu Lys Ala Glu Gln Thr Ile Leu Pro Leu Val Asp Glu
185                1190                1195                1200

Ala Leu Gln His Thr Thr Thr Lys Gly Ile Val Phe Gln His Pro Glu
               1205                1210                1215

Ile Val Ala His Met Asp Leu Met Arg Glu Asp Leu His Leu Glu Pro
            1220                1225                1230

Phe Tyr Trp Lys Leu Pro Glu Gln Phe Glu Gly Lys Lys Leu Met Ala
       1235                1240                1245

Tyr Gly Gly Lys Leu Lys Tyr Ala Ile Tyr Phe Glu Ala Arg Glu Glu
   1250                1255                1260

Thr Gly Phe Ser Thr Tyr Asn Pro Gln Val Ile Ile Arg Gly Gly Thr
265                1270                1275                1280

Pro Thr His Ala Arg Ile Ile Val Arg His Met Ala Ala Pro Leu Ile
               1285                1290                1295

Gly Gln Leu Thr Arg His Glu Ile Glu Met Thr Glu Lys Glu Trp Lys
            1300                1305                1310
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Tyr Tyr Gly Asp Asp Pro Arg Val His Arg Thr Val Thr Arg Glu Asp
      1315                1320                1325

Phe Leu Asp Ile Leu Tyr Asp Ile His Tyr Ile Leu Ile Lys Ala Thr
   1330                1335                1340

Tyr Gly Asn Phe Met Arg Gln Ser Arg Ile Ser Glu Ile Ser Met Glu
345                1350                1355                1360

Val Ala Glu Gln Gly Arg Gly Thr Thr Met Thr Pro Pro Ala Asp Leu
               1365                1370                1375

Ile Glu Lys Cys Asp Cys Pro Leu Gly Tyr Ser Gly Leu Ser Cys Glu
            1380                1385                1390

Ala Cys Leu Pro Gly Phe Tyr Arg Leu Arg Ser Gln Pro Gly Gly Arg
      1395                1400                1405

Thr Pro Gly Pro Thr Leu Gly Thr Cys Val Pro Cys Gln Cys Asn Gly
   1410                1415                1420

His Ser Ser Leu Cys Asp Pro Glu Thr Ser Ile Cys Gln Asn Cys Gln
425                1430                1435                1440

His His Thr Ala Gly Asp Phe Cys Glu Arg Cys Ala Leu Gly Tyr Tyr
               1445                1450                1455

Gly Ile Val Lys Gly Leu Pro Asn Asp Cys Gln Gln Cys Ala Cys Pro
            1460                1465                1470

Leu Ile Ser Ser Ser Asn Asn Phe Ser Pro Ser Cys Val Ala Glu Gly
      1475                1480                1485

Leu Asp Asp Tyr Arg Cys Thr Ala Cys Pro Arg Gly Tyr Glu Gly Gln
   1490                1495                1500

Tyr Cys Glu Arg Cys Ala Pro Gly Tyr Thr Gly Ser Pro Gly Asn Pro
505                1510                1515                1520

Gly Gly Ser Cys Gln Glu Cys Glu Cys Asp Pro Tyr Gly Ser Leu Pro
               1525                1530                1535

Val Pro Cys Asp Pro Val Thr Gly Phe Cys Thr Cys Arg Pro Gly Ala
            1540                1545                1550

Thr Gly Arg Lys Cys Asp Gly Cys Lys His Trp His Ala Arg Glu Gly
      1555                1560                1565

Trp Glu Cys Val Phe Cys Gly Asp Glu Cys Thr Gly Leu Leu Leu Gly
   1570                1575                1580

Asp Leu Ala Arg Leu Glu Gln Met Val Met Ser Ile Asn Leu Thr Gly
585                1590                1595                1600

Pro Leu Pro Ala Pro Tyr Lys Met Leu Tyr Gly Leu Glu Asn Met Thr
               1605                1610                1615

Gln Glu Leu Lys His Leu Leu Ser Pro Gln Arg Ala Pro Glu Arg Leu
            1620                1625                1630
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Ile Gln Leu Ala Glu Gly Asn Leu Asn Thr Leu Val Thr Glu Met Asn
       1635                1640                1645

Glu Leu Leu Thr Arg Ala Thr Lys Val Thr Ala Asp Gly Glu Gln Thr
   1650                1655                1660

Gly Gln Asp Ala Glu Arg Thr Asn Thr Arg Ala Lys Ser Leu Gly Glu
665                1670                1675                1680

Phe Ile Lys Glu Leu Ala Arg Asp Ala Glu Ala Val Asn Glu Lys Ala
               1685                1690                1695

Ile Lys Leu Asn Glu Thr Leu Gly Thr Arg Asp Glu Ala Phe Glu Arg
            1700                1705                1710

Asn Leu Glu Gly Leu Gln Lys Glu Ile Asp Gln Met Ile Lys Glu Leu
       1715                1720                1725

Arg Arg Lys Asn Leu Glu Thr Gln Lys Glu Ile Ala Glu Asp Glu Leu
   1730                1735                1740

Val Ala Ala Glu Ala Leu Leu Lys Lys Val Lys Lys Leu Phe Gly Glu
745                1750                1755                1760

Ser Arg Gly Glu Asn Glu Glu Met Glu Lys Asp Leu Arg Glu Lys Leu
               1765                1770                1775

Ala Asp Tyr Lys Asn Lys Val Asp Asp Ala Trp Asp Leu Leu Arg Glu
            1780                1785                1790

Ala Thr Asp Lys Ile Arg Glu Ala Asn Arg Leu Phe Ala Val Asn Gln
       1795                1800                1805

Lys Asn Met Thr Ala Leu Glu Lys Lys Lys Glu Ala Val Glu Ser Gly
   1810                1815                1820

Lys Arg Gln Ile Glu Asn Thr Leu Lys Glu Gly Asn Asp Ile Leu Asp
825                1830                1835                1840

Glu Ala Asn Arg Leu Ala Asp Glu Ile Asn Ser Ile Ile Asp Tyr Val
               1845                1850                1855

Glu Asp Ile Gln Thr Lys Leu Pro Pro Met Ser Glu Glu Leu Asn Asp
            1860                1865                1870

Lys Ile Asp Asp Leu Ser Gln Glu Ile Lys Asp Arg Lys Leu Ala Glu
       1875                1880                1885

Lys Val Ser Gln Ala Glu Ser His Ala Ala Gln Leu Asn Asp Ser Ser
   1890                1895                1900

Ala Val Leu Asp Gly Ile Leu Asp Glu Ala Lys Asn Ile Ser Phe Asn
905                1910                1915                1920

Ala Thr Ala Ala Phe Lys Ala Tyr Ser Asn Ile Lys Asp Tyr Ile Asp
               1925                1930                1935

Glu Ala Glu Lys Val Ala Lys Glu Ala Lys Asp Leu Ala His Glu Ala
            1940                1945                1950

Thr Lys Leu Ala Thr Gly Pro Arg Gly Leu Leu Lys Glu Asp Ala Lys
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      1955                1960                1965

Gly Cys Leu Gln Lys Ser Phe Arg Ile Leu Asn Glu Ala Lys Lys Leu
   1970                1975                1980

Ala Asn Asp Val Lys Glu Asn Glu Asp His Leu Asn Gly Leu Lys Thr
985                1990                1995                2000

Arg Ile Glu Asn Ala Asp Ala Arg Asn Gly Asp Leu Leu Arg Thr Leu
               2005                2010                2015

Asn Asp Thr Leu Gly Lys Leu Ser Ala Ile Pro Asn Asp Thr Ala Ala
            2020                2025                2030

Lys Leu Gln Ala Val Lys Asp Lys Ala Arg Gln Ala Asn Asp Thr Ala
       2035                2040                2045

Lys Asp Val Leu Ala Gln Ile Thr Glu Leu His Gln Asn Leu Asp Gly
   2050                2055                2060

Leu Lys Lys Asn Tyr Asn Lys Leu Ala Asp Ser Val Ala Lys Thr Asn
065                2070                2075                2080

Ala Val Val Lys Asp Pro Ser Lys Asn Lys Ile Ile Ala Asp Ala Asp
               2085                2090                2095

Ala Thr Val Lys Asn Leu Glu Gln Glu Ala Asp Arg Leu Ile Asp Lys
            2100                2105                2110

Leu Lys Pro Ile Lys Glu Leu Glu Asp Asn Leu Lys Lys Asn Ile Ser
       2115                2120                2125

Glu Ile Lys Glu Leu Ile Asn Gln Ala Arg Lys Gln Ala Asn Ser Ile
   2130                2135                2140

Lys Val Ser Val Ser Ser Gly Gly Asp Cys Ile Arg Thr Tyr Lys Pro
145                2150                2155                2160

Glu Ile Lys Lys Gly Ser Tyr Asn Asn Ile Val Val Asn Val Lys Thr
               2165                2170                2175

Ala Val Ala Asp Asn Leu Leu Phe Tyr Leu Gly Ser Ala Lys Phe Ile
            2180                2185                2190

Asp Phe Leu Ala Ile Glu Met Arg Lys Gly Lys Val Ser Phe Leu Trp
       2195                2200                2205

Asp Val Gly Ser Gly Val Gly Arg Val Glu Tyr Pro Asp Leu Thr Ile
   2210                2215                2220

Asp Asp Ser Tyr Trp Tyr Arg Ile Val Ala Ser Arg Thr Gly Arg Asn
225                2230                2235                2240

Gly Thr Ile Ser Val Arg Ala Leu Asp Gly Pro Lys Ala Ser Ile Val
               2245                2250                2255

Pro Ser Thr His His Ser Thr Ser Pro Pro Gly Tyr Thr Ile Leu Asp
            2260                2265                2270

Val Asp Ala Asn Ala Met Leu Phe Val Gly Gly Leu Thr Gly Lys Leu
       2275                2280                2285
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Lys Lys Ala Asp Ala Val Arg Val Ile Thr Phe Thr Gly Cys Met Gly
   2290                2295                2300

Glu Thr Tyr Phe Asp Asn Lys Pro Ile Gly Leu Trp Asn Phe Arg Glu
305                 2310                2315                2320

Lys Glu Gly Asp Cys Lys Gly Cys Thr Val Ser Pro Gln Val Glu Asp
                2325                2330                2335

Ser Glu Gly Thr Ile Gln Phe Asp Gly Glu Gly Tyr Ala Leu Val Ser
            2340                2345                2350

Arg Pro Ile Arg Trp Tyr Pro Asn Ile Ser Thr Val Met Phe Lys Phe
        2355                2360                2365

Arg Thr Phe Ser Ser Ser Ala Leu Leu Met Tyr Leu Ala Thr Arg Asp
    2370                2375                2380

Leu Arg Asp Phe Met Ser Val Glu Leu Thr Asp Gly His Ile Lys Val
385                 2390                2395                2400

Ser Tyr Asp Leu Gly Ser Gly Met Ala Ser Val Val Ser Asn Gln Asn
                2405                2410                2415

His Asn Asp Gly Lys Trp Lys Ser Phe Thr Leu Ser Arg Ile Gln Lys
            2420                2425                2430

Gln Ala Asn Ile Ser Ile Val Asp Ile Asp Thr Asn Gln Glu Glu Asn
        2435                2440                2445

Ile Ala Thr Ser Ser Ser Gly Asn Asn Phe Gly Leu Asp Leu Lys Ala
    2450                2455                2460

Asp Asp Lys Ile Tyr Phe Gly Gly Leu Pro Thr Leu Arg Asn Leu Ser
465                 2470                2475                2480

Met Lys Ala Arg Pro Glu Val Asn Leu Lys Lys Tyr Ser Gly Cys Leu
                2485                2490                2495

Lys Asp Ile Glu Ile Ser Arg Thr Pro Tyr Asn Ile Leu Ser Ser Pro
            2500                2505                2510

Asp Tyr Val Gly Val Thr Lys Gly Cys Ser Leu Glu Asn Val Tyr Thr
        2515                2520                2525

Val Ser Phe Pro Lys Pro Gly Phe Val Glu Leu Ser Pro Val Pro Ile
    2530                2535                2540

Asp Val Gly Thr Glu Ile Asn Leu Ser Phe Ser Thr Lys Asn Glu Ser
545                 2550                2555                2560

Gly Ile Ile Leu Leu Gly Ser Gly Gly Thr Pro Ala Pro Pro Arg Arg
                2565                2570                2575

Lys Arg Arg Gln Thr Gly Gln Ala Tyr Tyr Val Ile Leu Leu Asn Arg
            2580                2585                2590

Gly Arg Leu Glu Val His Leu Ser Thr Gly Ala Arg Thr Met Arg Lys
        2595                2600                2605
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Ile Val Ile Arg Pro Glu Pro Asn Leu Phe His Asp Gly Arg Glu His
2610 2615 2620

Ser Val His Val Glu Arg Thr Arg Gly Ile Phe Thr Val Gln Val Asp
625 2630 2635 2640

Glu Asn Arg Arg Tyr Met Gln Asn Leu Thr Val Glu Gln Pro Ile Glu
2645 2650 2655

Val Lys Lys Leu Phe Val Gly Gly Ala Pro Pro Glu Phe Gln Pro Ser
2660 2665 2670

Pro Leu Arg Asn Ile Pro Pro Phe Glu Gly Cys Ile Trp Asn Leu Val
2675 2680 2685

Ile Asn Ser Val Pro Met Asp Phe Ala Arg Pro Val Ser Phe Lys Asn
2690 2695 2700

Ala Asp Ile Gly Arg Cys Ala His Gln Lys Leu Arg Glu Asp Glu Asp
705 2710 2715 2720

Gly Ala Ala Pro Ala Glu Ile Val Ile Gln Pro Glu Pro Val Pro Thr
2725 2730 2735

Pro Ala Phe Pro Thr Pro Thr Pro Val Leu Thr His Gly Pro Cys Ala
2740 2745 2750

Ala Glu Ser Glu Pro Ala Leu Leu Ile Gly Ser Lys Gln Phe Gly Leu
2755 2760 2765

Ser Arg Asn Ser His Ile Ala Ile Ala Phe Asp Asp Thr Lys Val Lys
2770 2775 2780

Asn Arg Leu Thr Ile Glu Leu Glu Val Arg Thr Glu Ala Glu Ser Gly
785 2790 2795 2800

Leu Leu Phe Tyr Met Ala Ala Ile Asn His Ala Asp Phe Ala Thr Val
2805 2810 2815

Gln Leu Arg Asn Gly Leu Pro Tyr Phe Ser Tyr Asp Leu Gly Ser Gly
2820 2825 2830

Asp Thr His Thr Met Ile Pro Thr Lys Ile Asn Asp Gly Gln Trp His
2835 2840 2845

Lys Ile Lys Ile Met Arg Ser Lys Gln Glu Gly Ile Leu Tyr Val Asp
2850 2855 2860

Gly Ala Ser Asn Arg Thr Ile Ser Pro Lys Lys Ala Asp Ile Leu Asp
865 2870 2875 2880

Val Val Gly Met Leu Tyr Val Gly Gly Leu Pro Ile Asn Tyr Thr Thr
2885 2890 2895

Arg Arg Ile Gly Pro Val Thr Tyr Ser Ile Asp Gly Cys Val Arg Asn
2900 2905 2910

Leu His Met Ala Glu Ala Pro Ala Asp Leu Glu Gln Pro Thr Ser Ser
2915 2920 2925

Phe His Val Gly Thr Cys Phe Ala Asn Ala Gln Arg Gly Thr Tyr Phe

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   2930                2935                2940

Asp Gly Thr Gly Phe Ala Lys Ala Val Gly Gly Phe Lys Val Gly Leu
945                2950                2955                2960

Asp Leu Leu Val Glu Phe Glu Phe Ala Thr Thr Thr Thr Thr Gly Val
               2965                2970                2975

Leu Leu Gly Ile Ser Ser Gln Lys Met Asp Gly Met Gly Ile Glu Met
            2980                2985                2990

Ile Asp Glu Lys Leu Met Phe His Val Asp Asn Gly Ala Gly Arg Phe
       2995                3000                3005

Thr Ala Val Tyr Asp Ala Gly Val Pro Gly His Leu Cys Asp Gly Gln
   3010                3015                3020

Trp His Lys Val Thr Ala Asn Lys Ile Lys His Arg Ile Glu Leu Thr
025                3030                3035                3040

Val Asp Gly Asn Gln Val Glu Ala Gln Ser Pro Asn Pro Ala Ser Thr
               3045                3050                3055

Ser Ala Asp Thr Asn Asp Pro Val Phe Val Gly Gly Phe Pro Asp Asp
            3060                3065                3070

Leu Lys Gln Phe Gly Leu Thr Thr Ser Ile Pro Phe Arg Gly Cys Ile
       3075                3080                3085

Arg Ser Leu Lys Leu Thr Lys Gly Thr Ala Ser His Trp Arg Leu Ile
   3090                3095                3100

Leu Pro Arg Pro Trp Asn
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cag cgg ccg cag cag cag cgg cag tca cag gca cat cag caa aga ggt   48
Gln Arg Pro Gln Gln Gln Arg Gln Ser Gln Ala His Gln Gln Arg Gly
  1               5                  10                  15

tta ttc cct gct gtc ctg aat ctt gct tct aat gct ctt atc acg acc   96
Leu Phe Pro Ala Val Leu Asn Leu Ala Ser Asn Ala Leu Ile Thr Thr
             20                  25                  30

aat gca aca tgt gga gaa aaa gga cct gaa atg tac tgc aaa ttg gta   144
Asn Ala Thr Cys Gly Glu Lys Gly Pro Glu Met Tyr Cys Lys Leu Val
         35                  40                  45

gaa cat gtc cct ggg cag cct gtg agg aac ccg cag tgt cga atc tgc   192
Glu His Val Pro Gly Gln Pro Val Arg Asn Pro Gln Cys Arg Ile Cys
     50                  55                  60
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aat caa aac agc agc aat cca aac cag aga cac ccg att aca aat gct   240
Asn Gln Asn Ser Ser Asn Pro Asn Gln Arg His Pro Ile Thr Asn Ala
 65                  70                  75                  80

att gat gga aag aac act tgg tgg cag agt ccc agt att aag aat gga   288
Ile Asp Gly Lys Asn Thr Trp Trp Gln Ser Pro Ser Ile Lys Asn Gly
                85                  90                  95

atc gaa tac cat tat gtg aca att aca ctg gat tta cag cag gtg ttc   336
Ile Glu Tyr His Tyr Val Thr Ile Thr Leu Asp Leu Gln Gln Val Phe
            100                 105                 110

cag atc gcg tat gtg att gtg aag gca gct aac tcc ccc cgg cct gga   384
Gln Ile Ala Tyr Val Ile Val Lys Ala Ala Asn Ser Pro Arg Pro Gly
        115                 120                 125

aac tgg att ttg gaa cgc tct ctt gat gat gtt gaa tac aag ccc tgg   432
Asn Trp Ile Leu Glu Arg Ser Leu Asp Asp Val Glu Tyr Lys Pro Trp
    130                 135                 140

cag tat cat gct gtg aca gac acg gag tgc cta acg ctt tac aat att   480
Gln Tyr His Ala Val Thr Asp Thr Glu Cys Leu Thr Leu Tyr Asn Ile
145                 150                 155                 160

tat ccc cgc act ggg cca ccg tca tat gcc aaa gat gat gag gtc atc   528
Tyr Pro Arg Thr Gly Pro Pro Ser Tyr Ala Lys Asp Asp Glu Val Ile
                165                 170                 175

tgc act tca ttt tac tcc aag ata cac ccc tta gaa aat gga gag att   576
Cys Thr Ser Phe Tyr Ser Lys Ile His Pro Leu Glu Asn Gly Glu Ile
            180                 185                 190

cac atc tct tta atc aat ggg aga cca agt gcc gat gat cct tct cca   624
His Ile Ser Leu Ile Asn Gly Arg Pro Ser Ala Asp Asp Pro Ser Pro
        195                 200                 205

gaa ctg cta gaa ttt acc tcc gct cgc tat att cgc ctg aga ttt cag   672
Glu Leu Leu Glu Phe Thr Ser Ala Arg Tyr Ile Arg Leu Arg Phe Gln
    210                 215                 220

agg atc cgc aca ctg aat gct gac ttg atg atg ttt gct cac aaa gac   720
Arg Ile Arg Thr Leu Asn Ala Asp Leu Met Met Phe Ala His Lys Asp
225                 230                 235                 240

cca aga gaa att gac ccc att gtc acc aga aga tat tac tac tcg gtc   768
Pro Arg Glu Ile Asp Pro Ile Val Thr Arg Arg Tyr Tyr Tyr Ser Val
                245                 250                 255

aag gat att tca gtt gga ggg atg tgc atc tgc tat ggt cat gcc agg   816
Lys Asp Ile Ser Val Gly Gly Met Cys Ile Cys Tyr Gly His Ala Arg
            260                 265                 270

gct tgt cca ctt gat cca gcg aca aat aaa tct cgc tgt gag tgt gag   864
Ala Cys Pro Leu Asp Pro Ala Thr Asn Lys Ser Arg Cys Glu Cys Glu
        275                 280                 285

cat aac aca tgt ggc gat agc tgt gat cag tgc tgt cca gga ttc cat   912
His Asn Thr Cys Gly Asp Ser Cys Asp Gln Cys Cys Pro Gly Phe His
    290                 295                 300
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cag aaa ccc tgg aga gct gga act ttt cta act aaa act gaa tgt gaa   960
Gln Lys Pro Trp Arg Ala Gly Thr Phe Leu Thr Lys Thr Glu Cys Glu
305                 310                 315                 320

gca tgc aat tgt cat gga aaa gct gaa gaa tgc tat tat gat gaa aat   1008
Ala Cys Asn Cys His Gly Lys Ala Glu Glu Cys Tyr Tyr Asp Glu Asn
                325                 330                 335

gtt gcc aga aga aat ctg agt ttg aat ata cgt gga aag tac att gga   1056
Val Ala Arg Arg Asn Leu Ser Leu Asn Ile Arg Gly Lys Tyr Ile Gly
            340                 345                 350

ggg ggt gtc tgc att aat tgt acc caa aac act gct ggt ata aac tgc   1104
Gly Gly Val Cys Ile Asn Cys Thr Gln Asn Thr Ala Gly Ile Asn Cys
        355                 360                 365

gag aca tgt aca gat ggc ttc ttc aga ccc aaa ggg gta tct cca aat   1152
Glu Thr Cys Thr Asp Gly Phe Phe Arg Pro Lys Gly Val Ser Pro Asn
    370                 375                 380

tat cca agg cca tgc cag cca tgt cat tgc gat cca att ggt tcc tta   1200
Tyr Pro Arg Pro Cys Gln Pro Cys His Cys Asp Pro Ile Gly Ser Leu
385                 390                 395                 400

aat gaa gtc tgt gtc aag gat gag aaa cat gct cga cga ggt ttg gca   1248
Asn Glu Val Cys Val Lys Asp Glu Lys His Ala Arg Arg Gly Leu Ala
                405                 410                 415

cct gga tcc tgt cat tgc aaa act ggt ttt gga ggt gtg agc tgt gat   1296
Pro Gly Ser Cys His Cys Lys Thr Gly Phe Gly Gly Val Ser Cys Asp
            420                 425                 430

cgg tgt gcc agg ggc tac act ggc tac ccg gac tgc aaa gcc tgt aac   1344
Arg Cys Ala Arg Gly Tyr Thr Gly Tyr Pro Asp Cys Lys Ala Cys Asn
        435                 440                 445

tgc agt ggg tta ggg agc aaa aat gag gat cct tgt ttt ggc ccc tgt   1392
Cys Ser Gly Leu Gly Ser Lys Asn Glu Asp Pro Cys Phe Gly Pro Cys
    450                 455                 460

atc tgc aag gaa aat gtt gaa gga gga gac tgt agt cgt tgc aaa tcc   1440
Ile Cys Lys Glu Asn Val Glu Gly Gly Asp Cys Ser Arg Cys Lys Ser
465                 470                 475                 480

ggc ttc ttc aat ttg caa gag gat aat tgg aaa ggc tgc gat gag tgt   1488
Gly Phe Phe Asn Leu Gln Glu Asp Asn Trp Lys Gly Cys Asp Glu Cys
                485                 490                 495

ttc tgt tca ggg gtt tca aac aga tgt cag agt tcc tac tgg acc tat   1536
Phe Cys Ser Gly Val Ser Asn Arg Cys Gln Ser Ser Tyr Trp Thr Tyr
            500                 505                 510

ggc aaa ata caa gat atg agt ggc tgg tat ctg act gac ctt cct ggc   1584
Gly Lys Ile Gln Asp Met Ser Gly Trp Tyr Leu Thr Asp Leu Pro Gly
        515                 520                 525

cgc att cga gtg gct ccc cag cag gac gac ttg gac tca cct cag cag   1632
Arg Ile Arg Val Ala Pro Gln Gln Asp Asp Leu Asp Ser Pro Gln Gln
    530                 535                 540

atc agc atc agt aac gcg gag gcc cgg caa gcc ctg ccg cac agc tac   1680
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Ile Ser Ile Ser Asn Ala Glu Ala Arg Gln Ala Leu Pro His Ser Tyr
545                 550                 555                 560

tac tgg agc gcg ccg gct ccc tat ctg gga aac aaa ctc cca gca gta   1728
Tyr Trp Ser Ala Pro Ala Pro Tyr Leu Gly Asn Lys Leu Pro Ala Val
                565                 570                 575

gga gga cag ttg aca ttt acc ata tca tat gac ctt gaa gaa gag gaa   1776
Gly Gly Gln Leu Thr Phe Thr Ile Ser Tyr Asp Leu Glu Glu Glu Glu
            580                 585                 590

gaa gat aca gaa cgt gtt ctc cag ctt atg att atc tta gag ggt aat   1824
Glu Asp Thr Glu Arg Val Leu Gln Leu Met Ile Ile Leu Glu Gly Asn
        595                 600                 605

gac ttg agc atc agc aca gcc caa gat gag gtg tac ctg cac cca tct   1872
Asp Leu Ser Ile Ser Thr Ala Gln Asp Glu Val Tyr Leu His Pro Ser
    610                 615                 620

gaa gaa cat act aat gta ttg tta ctt aaa gaa gaa tca ttt acc ata   1920
Glu Glu His Thr Asn Val Leu Leu Leu Lys Glu Glu Ser Phe Thr Ile
625                 630                 635                 640

cat ggc aca cat ttt cca gtc cgt aga aag gaa ttt atg aca gtg ctt   1968
His Gly Thr His Phe Pro Val Arg Arg Lys Glu Phe Met Thr Val Leu
                645                 650                 655

gcg aat ttg aag aga gtc ctc cta caa atc aca tac agc ttt ggg atg   2016
Ala Asn Leu Lys Arg Val Leu Leu Gln Ile Thr Tyr Ser Phe Gly Met
            660                 665                 670

gat gcc atc ttc agg ttg agc tct gtt aac ctt gaa tcc gct gtc tcc   2064
Asp Ala Ile Phe Arg Leu Ser Ser Val Asn Leu Glu Ser Ala Val Ser
        675                 680                 685

tat cct act gat gga agc att gca gca gct gta gaa gtg tgt cag tgc   2112
Tyr Pro Thr Asp Gly Ser Ile Ala Ala Ala Val Glu Val Cys Gln Cys
    690                 695                 700

cca cca ggg tat act ggc tcc tct tgt gaa tct tgt tgg cct agg cac   2160
Pro Pro Gly Tyr Thr Gly Ser Ser Cys Glu Ser Cys Trp Pro Arg His
705                 710                 715                 720

agg cga gtt aac ggc act att ttt ggt ggc atc tgt gag cca tgt cag   2208
Arg Arg Val Asn Gly Thr Ile Phe Gly Gly Ile Cys Glu Pro Cys Gln
                725                 730                 735

tgc ttt ggt cat gcg gag tcc tgt gat gac gtc act gga gaa tgc ctg   2256
Cys Phe Gly His Ala Glu Ser Cys Asp Asp Val Thr Gly Glu Cys Leu
            740                 745                 750

aac tgt aag gat cac aca ggt ggc cca tat tgt gat aaa tgt ctt cct   2304
Asn Cys Lys Asp His Thr Gly Gly Pro Tyr Cys Asp Lys Cys Leu Pro
        755                 760                 765

ggt ttc tat ggc gag cct act aaa gga acc tct gaa gac tgt caa ccc   2352
Gly Phe Tyr Gly Glu Pro Thr Lys Gly Thr Ser Glu Asp Cys Gln Pro
    770                 775                 780

tgt gcc tgt cca ctc aat atc cca tcc aat aac ttt agc cca acg tgc   2400
Cys Ala Cys Pro Leu Asn Ile Pro Ser Asn Asn Phe Ser Pro Thr Cys
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785                 790                 795                 800

cat tta gac cgg agt ctt gga ttg atc tgt gat gga tgc cct gtc ggg   2448
His Leu Asp Arg Ser Leu Gly Leu Ile Cys Asp Gly Cys Pro Val Gly
                805                 810                 815

tac aca gga cca cgc tgt gag agg tgt gca gaa ggc tat ttt gga caa   2496
Tyr Thr Gly Pro Arg Cys Glu Arg Cys Ala Glu Gly Tyr Phe Gly Gln
            820                 825                 830

ccc tct gta cct gga gga tca tgt cag cca tgc caa tgc aat gac aac   2544
Pro Ser Val Pro Gly Gly Ser Cys Gln Pro Cys Gln Cys Asn Asp Asn
        835                 840                 845

ctt gac ttc tcc atc cct ggc agc tgt gac agc ttg tct ggc tcc tgt   2592
Leu Asp Phe Ser Ile Pro Gly Ser Cys Asp Ser Leu Ser Gly Ser Cys
    850                 855                 860

ctg ata tgt aaa cca ggt aca aca ggc cgg tac tgt gag ctc tgt gct   2640
Leu Ile Cys Lys Pro Gly Thr Thr Gly Arg Tyr Cys Glu Leu Cys Ala
865                 870                 875                 880

gat gga tat ttt gga gat gca gtt gat gcg aag aac tgt cag ccc tgt   2688
Asp Gly Tyr Phe Gly Asp Ala Val Asp Ala Lys Asn Cys Gln Pro Cys
                885                 890                 895

cgc tgt aat gcc ggt ggc tct ttc tct gag gtt tgc cac agt caa act   2736
Arg Cys Asn Ala Gly Gly Ser Phe Ser Glu Val Cys His Ser Gln Thr
            900                 905                 910

gga cag tgt gag tgc aga gcc aac gtt cag ggt cag aga tgt gac aaa   2784
Gly Gln Cys Glu Cys Arg Ala Asn Val Gln Gly Gln Arg Cys Asp Lys
        915                 920                 925

tgc aag gct ggg acc ttt ggc cta caa tca gca agg ggc tgt gtt ccc   2832
Cys Lys Ala Gly Thr Phe Gly Leu Gln Ser Ala Arg Gly Cys Val Pro
    930                 935                 940

tgc aac tgc aat tct ttt ggg tct aag tca ttc gac tgt gaa gag agt   2880
Cys Asn Cys Asn Ser Phe Gly Ser Lys Ser Phe Asp Cys Glu Glu Ser
945                 950                 955                 960

gga caa tgt tgg tgc caa cct gga gtc aca ggg aag aaa tgt gac cgc   2928
Gly Gln Cys Trp Cys Gln Pro Gly Val Thr Gly Lys Lys Cys Asp Arg
                965                 970                 975

tgt gcc cac ggc tat ttc aac ttc caa gaa gga ggc tgc aca gct tgt   2976
Cys Ala His Gly Tyr Phe Asn Phe Gln Glu Gly Gly Cys Thr Ala Cys
            980                 985                 990

gaa tgt tct cat ctg ggt aat aat tgt gac cca aag act ggg cga tgc   3024
Glu Cys Ser His Leu Gly Asn Asn Cys Asp Pro Lys Thr Gly Arg Cys
        995                1000                1005

att tgc cca ccc aat acc att gga gag aaa tgt tct aaa tgt gca ccc   3072
Ile Cys Pro Pro Asn Thr Ile Gly Glu Lys Cys Ser Lys Cys Ala Pro
   1010                1015                1020

aat acc tgg ggc cac agc att acc act ggt tgt aag gct tgt aac tgc   3120
Asn Thr Trp Gly His Ser Ile Thr Thr Gly Cys Lys Ala Cys Asn Cys
1025                1030                1035                1040
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agc aca gtg gga tcc ttg gat ttc caa tgc aat gta aat aca ggc caa   3168
Ser Thr Val Gly Ser Leu Asp Phe Gln Cys Asn Val Asn Thr Gly Gln
                1045                1050                1055

tgc aac tgt cat cca aaa ttc tct ggt gca aaa tgt aca gag tgc agt   3216
Cys Asn Cys His Pro Lys Phe Ser Gly Ala Lys Cys Thr Glu Cys Ser
            1060                1065                1070

cga ggt cac tgg aac tac cct cgc tgc aat ctc tgt gac tgc ttc ctc   3264
Arg Gly His Trp Asn Tyr Pro Arg Cys Asn Leu Cys Asp Cys Phe Leu
        1075                1080                1085

cct ggg aca gat gcc aca acc tgt gat tca gag act aaa aaa tgc tcc   3312
Pro Gly Thr Asp Ala Thr Thr Cys Asp Ser Glu Thr Lys Lys Cys Ser
    1090                1095                1100

tgt agt gat caa act ggg cag tgc act tgt aag gtg aat gtg gaa ggc   3360
Cys Ser Asp Gln Thr Gly Gln Cys Thr Cys Lys Val Asn Val Glu Gly
1105                1110                1115                1120

atc cac tgt gac aga tgc cgg cct ggc aaa ttc gga ctc gat gcc aag   3408
Ile His Cys Asp Arg Cys Arg Pro Gly Lys Phe Gly Leu Asp Ala Lys
                1125                1130                1135

aat cca ctt ggc tgc agc agc tgc tat tgc ttc ggc act act acc cag   3456
Asn Pro Leu Gly Cys Ser Ser Cys Tyr Cys Phe Gly Thr Thr Thr Gln
            1140                1145                1150

tgc tct gaa gca aaa gga ctg atc cgg acg tgg gtg act ctg aag gct   3504
Cys Ser Glu Ala Lys Gly Leu Ile Arg Thr Trp Val Thr Leu Lys Ala
        1155                1160                1165

gag cag acc att cta ccc ctg gta gat gag gct ctg cag cac acg acc   3552
Glu Gln Thr Ile Leu Pro Leu Val Asp Glu Ala Leu Gln His Thr Thr
    1170                1175                1180

acc aag ggc att gtt ttt caa cat cca gag att gtt gcc cac atg gac   3600
Thr Lys Gly Ile Val Phe Gln His Pro Glu Ile Val Ala His Met Asp
1185                1190                1195                1200

ctg atg aga gaa gat ctc cat ttg gaa cct ttt tat tgg aaa ctt cca   3648
Leu Met Arg Glu Asp Leu His Leu Glu Pro Phe Tyr Trp Lys Leu Pro
                1205                1210                1215

gaa caa ttt gaa gga aag aag ttg atg gcc tat ggg ggc aaa ctc aag   3696
Glu Gln Phe Glu Gly Lys Lys Leu Met Ala Tyr Gly Gly Lys Leu Lys
            1220                1225                1230

tat gca atc tat ttc gag gct cgg gaa gaa aca ggt ttc tct aca tat   3744
Tyr Ala Ile Tyr Phe Glu Ala Arg Glu Glu Thr Gly Phe Ser Thr Tyr
        1235                1240                1245

aat cct caa gtg atc att cga ggt ggg aca cct act cat gct aga att   3792
Asn Pro Gln Val Ile Ile Arg Gly Gly Thr Pro Thr His Ala Arg Ile
    1250                1255                1260

atc gtc agg cat atg gct gct cct ctg att ggc caa ttg aca agg cat   3840
Ile Val Arg His Met Ala Ala Pro Leu Ile Gly Gln Leu Thr Arg His
1265                1270                1275                1280
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gaa att gaa atg aca gag aaa gaa tgg aaa tat tat ggg gat gat cct   3888
Glu Ile Glu Met Thr Glu Lys Glu Trp Lys Tyr Tyr Gly Asp Asp Pro
             1285                1290                1295

cga gtc cat aga act gtg acc cga gaa gac ttc ttg gat ata cta tat   3936
Arg Val His Arg Thr Val Thr Arg Glu Asp Phe Leu Asp Ile Leu Tyr
          1300                1305                1310

gat att cat tac att ctt atc aaa gct act tat gga aat ttc atg cga   3984
Asp Ile His Tyr Ile Leu Ile Lys Ala Thr Tyr Gly Asn Phe Met Arg
       1315                1320                1325

caa agc agg att tct gaa atc tca atg gag gta gct gaa caa gga cgt   4032
Gln Ser Arg Ile Ser Glu Ile Ser Met Glu Val Ala Glu Gln Gly Arg
   1330                1335                1340

gga aca aca atg act cct cca gct gac ttg att gaa aaa tgt gat tgt   4080
Gly Thr Thr Met Thr Pro Pro Ala Asp Leu Ile Glu Lys Cys Asp Cys
1345                1350                1355                1360

ccc ctg ggc tat tct ggc ctg tcc tgt gag gca tgc ttg ccg gga ttt   4128
Pro Leu Gly Tyr Ser Gly Leu Ser Cys Glu Ala Cys Leu Pro Gly Phe
             1365                1370                1375

tat cga ctg cgt tct caa cca ggt ggc cgc acc cct gga cca acc ctg   4176
Tyr Arg Leu Arg Ser Gln Pro Gly Gly Arg Thr Pro Gly Pro Thr Leu
          1380                1385                1390

ggc acc tgt gtt cca tgt caa tgt aat gga cac agc agc ctg tgt gac   4224
Gly Thr Cys Val Pro Cys Gln Cys Asn Gly His Ser Ser Leu Cys Asp
       1395                1400                1405

cct gaa aca tcg ata tgc cag aat tgt caa cat cac act gct ggt gac   4272
Pro Glu Thr Ser Ile Cys Gln Asn Cys Gln His His Thr Ala Gly Asp
   1410                1415                1420

ttc tgt gaa cga tgt gct ctt gga tac tat gga att gtc aag gga ttg   4320
Phe Cys Glu Arg Cys Ala Leu Gly Tyr Tyr Gly Ile Val Lys Gly Leu
1425                1430                1435                1440

cca aat gac tgt cag caa tgt gcc tgc cct ctg att tct tcc agt aac   4368
Pro Asn Asp Cys Gln Gln Cys Ala Cys Pro Leu Ile Ser Ser Ser Asn
             1445                1450                1455

aat ttc agc ccc tct tgt gtc gca gaa gga ctt gac gac tac cgc tgc   4416
Asn Phe Ser Pro Ser Cys Val Ala Glu Gly Leu Asp Asp Tyr Arg Cys
          1460                1465                1470

acg gct tgt cca cgg gga tat gaa ggc cag tac tgt gaa agg tgt gcc   4464
Thr Ala Cys Pro Arg Gly Tyr Glu Gly Gln Tyr Cys Glu Arg Cys Ala
       1475                1480                1485

cct ggc tat act ggc agt cca ggc aac cct gga ggc tcc tgc caa gaa   4512
Pro Gly Tyr Thr Gly Ser Pro Gly Asn Pro Gly Gly Ser Cys Gln Glu
   1490                1495                1500

tgt gag tgt gat ccc tat ggc tca ctg cct gtg ccc tgt gac cct gtc   4560
Cys Glu Cys Asp Pro Tyr Gly Ser Leu Pro Val Pro Cys Asp Pro Val
1505                1510                1515                1520

aca gga ttc tgc acg tgc cga cct gga gcc acg gga agg aag tgt gac   4608
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Thr Gly Phe Cys Thr Cys Arg Pro Gly Ala Thr Gly Arg Lys Cys Asp
                1525                1530                1535

ggc tgc aag cac tgg cat gca cgc gag ggc tgg gag tgt gtt ttt tgt   4656
Gly Cys Lys His Trp His Ala Arg Glu Gly Trp Glu Cys Val Phe Cys
           1540                1545                1550

gga gat gag tgc act ggc ctt ctt ctc ggt gac ttg gct cgc ctg gag   4704
Gly Asp Glu Cys Thr Gly Leu Leu Leu Gly Asp Leu Ala Arg Leu Glu
       1555                1560                1565

cag atg gtc atg agc atc aac ctc act ggt ccg ctg cct gcg cca tat   4752
Gln Met Val Met Ser Ile Asn Leu Thr Gly Pro Leu Pro Ala Pro Tyr
   1570                1575                1580

aaa atg ctg tat ggt ctt gaa aat atg act cag gag cta aag cac ttg   4800
Lys Met Leu Tyr Gly Leu Glu Asn Met Thr Gln Glu Leu Lys His Leu
1585                1590                1595                1600

ctg tca cct cag cgg gcc cca gag agg ctt att cag ctg gca gag ggc   4848
Leu Ser Pro Gln Arg Ala Pro Glu Arg Leu Ile Gln Leu Ala Glu Gly
               1605                1610                1615

aat ctg aat aca ctc gtg acc gaa atg aac gag ctg ctg acc agg gct   4896
Asn Leu Asn Thr Leu Val Thr Glu Met Asn Glu Leu Leu Thr Arg Ala
           1620                1625                1630

acc aaa gtg aca gca gat ggc gag cag acc gga cag gat gct gag agg   4944
Thr Lys Val Thr Ala Asp Gly Glu Gln Thr Gly Gln Asp Ala Glu Arg
       1635                1640                1645

acc aac aca aga gca aag tcc ctg gga gaa ttc att aag gag ctt gcc   4992
Thr Asn Thr Arg Ala Lys Ser Leu Gly Glu Phe Ile Lys Glu Leu Ala
   1650                1655                1660

cgg gat gca gaa gct gta aat gaa aaa gct ata aaa cta aat gaa act   5040
Arg Asp Ala Glu Ala Val Asn Glu Lys Ala Ile Lys Leu Asn Glu Thr
1665                1670                1675                1680

cta gga act cga gac gag gcc ttt gag aga aat ttg gaa ggg ctt cag   5088
Leu Gly Thr Arg Asp Glu Ala Phe Glu Arg Asn Leu Glu Gly Leu Gln
               1685                1690                1695

aaa gag att gac cag atg att aaa gaa ctg agg agg aaa aat cta gag   5136
Lys Glu Ile Asp Gln Met Ile Lys Glu Leu Arg Arg Lys Asn Leu Glu
           1700                1705                1710

aca caa aag gaa att gct gaa gat gag ttg gta gct gca gaa gcc ctt   5184
Thr Gln Lys Glu Ile Ala Glu Asp Glu Leu Val Ala Ala Glu Ala Leu
       1715                1720                1725

ctg aaa aaa gtg aag aag ctg ttt gga gag tcc cgg ggg gaa aat gaa   5232
Leu Lys Lys Val Lys Lys Leu Phe Gly Glu Ser Arg Gly Glu Asn Glu
   1730                1735                1740

gaa atg gag aag gat ctc cgg gaa aaa ctg gct gac tac aaa aac aaa   5280
Glu Met Glu Lys Asp Leu Arg Glu Lys Leu Ala Asp Tyr Lys Asn Lys
1745                1750                1755                1760

gtt gat gat gct tgg gac ctt ttg aga gaa gcc aca gat aaa atc aga   5328
Val Asp Asp Ala Trp Asp Leu Leu Arg Glu Ala Thr Asp Lys Ile Arg
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                1765                1770                1775

gaa gct aat cgc cta ttt gca gta aat cag aaa aac atg act gca ttg   5376
Glu Ala Asn Arg Leu Phe Ala Val Asn Gln Lys Asn Met Thr Ala Leu
           1780                1785                1790

gag aaa aag aag gag gct gtt gag agc ggc aaa cga caa att gag aac   5424
Glu Lys Lys Lys Glu Ala Val Glu Ser Gly Lys Arg Gln Ile Glu Asn
       1795                1800                1805

act tta aaa gaa ggc aat gac ata ctc gat gaa gcc aac cgt ctt gca   5472
Thr Leu Lys Glu Gly Asn Asp Ile Leu Asp Glu Ala Asn Arg Leu Ala
   1810                1815                1820

gat gaa atc aac tcc atc ata gac tat gtt gaa gac atc caa act aaa   5520
Asp Glu Ile Asn Ser Ile Ile Asp Tyr Val Glu Asp Ile Gln Thr Lys
1825                1830                1835                1840

ttg cca cct atg tct gag gag ctt aat gat aaa ata gat gac ctc tcc   5568
Leu Pro Pro Met Ser Glu Glu Leu Asn Asp Lys Ile Asp Asp Leu Ser
               1845                1850                1855

caa gaa ata aag gac agg aag ctt gct gag aag gtg tcc cag gct gag   5616
Gln Glu Ile Lys Asp Arg Lys Leu Ala Glu Lys Val Ser Gln Ala Glu
           1860                1865                1870

agc cac gca gct cag ttg aat gac tca tct gct gtc ctt gat gga atc   5664
Ser His Ala Ala Gln Leu Asn Asp Ser Ser Ala Val Leu Asp Gly Ile
       1875                1880                1885

ctt gat gag gct aaa aac atc tcc ttc aat gcc act gca gcc ttc aaa   5712
Leu Asp Glu Ala Lys Asn Ile Ser Phe Asn Ala Thr Ala Ala Phe Lys
   1890                1895                1900

gct tac agc aat att aag gac tat att gat gaa gct gag aaa gtt gcc   5760
Ala Tyr Ser Asn Ile Lys Asp Tyr Ile Asp Glu Ala Glu Lys Val Ala
1905                1910                1915                1920

aaa gaa gcc aaa gat ctt gca cat gaa gct aca aaa ctg gca aca ggt   5808
Lys Glu Ala Lys Asp Leu Ala His Glu Ala Thr Lys Leu Ala Thr Gly
               1925                1930                1935

cct cgg ggt tta tta aag gaa gat gcc aaa ggc tgt ctt cag aaa agc   5856
Pro Arg Gly Leu Leu Lys Glu Asp Ala Lys Gly Cys Leu Gln Lys Ser
           1940                1945                1950

ttc agg att ctt aac gaa gcc aag aag tta gca aat gat gta aaa gaa   5904
Phe Arg Ile Leu Asn Glu Ala Lys Lys Leu Ala Asn Asp Val Lys Glu
       1955                1960                1965

aat gaa gac cat cta aat ggc tta aaa acc agg ata gaa aat gct gat   5952
Asn Glu Asp His Leu Asn Gly Leu Lys Thr Arg Ile Glu Asn Ala Asp
   1970                1975                1980

gct aga aat ggg gat ctc ttg aga act ttg aat gac act ttg gga aag   6000
Ala Arg Asn Gly Asp Leu Leu Arg Thr Leu Asn Asp Thr Leu Gly Lys
1985                1990                1995                2000

tta tca gct att cca aat gat aca gct gct aaa ctg caa gct gtt aag   6048
Leu Ser Ala Ile Pro Asn Asp Thr Ala Ala Lys Leu Gln Ala Val Lys
               2005                2010                2015
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gac aaa gcc aga caa gcc aac gac aca gct aaa gat gta ctg gca cag   6096
Asp Lys Ala Arg Gln Ala Asn Asp Thr Ala Lys Asp Val Leu Ala Gln
          2020                2025                2030

att aca gag ctc cac cag aac ctc gat ggc ctg aag aag aat tac aat   6144
Ile Thr Glu Leu His Gln Asn Leu Asp Gly Leu Lys Lys Asn Tyr Asn
       2035                2040                2045

aaa cta gca gac agc gtc gcc aaa acg aat gct gtg gtt aaa gat cct   6192
Lys Leu Ala Asp Ser Val Ala Lys Thr Asn Ala Val Val Lys Asp Pro
   2050                2055                2060

tcc aag aac aaa atc att gcc gat gca gat gcc act gtc aaa aat tta   6240
Ser Lys Asn Lys Ile Ile Ala Asp Ala Asp Ala Thr Val Lys Asn Leu
2065                2070                2075                2080

gaa cag gaa gct gac cgg cta ata gat aaa ctc aaa ccc atc aag gaa   6288
Glu Gln Glu Ala Asp Arg Leu Ile Asp Lys Leu Lys Pro Ile Lys Glu
               2085                2090                2095

ctt gag gat aac cta aag aaa aac atc tct gag ata aag gaa ttg ata   6336
Leu Glu Asp Asn Leu Lys Lys Asn Ile Ser Glu Ile Lys Glu Leu Ile
          2100                2105                2110

aac caa gct cgg aaa caa gcc aat tct atc aaa gta tct gtg tct tca   6384
Asn Gln Ala Arg Lys Gln Ala Asn Ser Ile Lys Val Ser Val Ser Ser
       2115                2120                2125

gga ggt gac tgc att cga aca tac aaa cca gaa atc aag aaa gga agt   6432
Gly Gly Asp Cys Ile Arg Thr Tyr Lys Pro Glu Ile Lys Lys Gly Ser
   2130                2135                2140

tac aat aat att gtt gtc aac gta aag aca gct gtt gct gat aac ctc   6480
Tyr Asn Asn Ile Val Val Asn Val Lys Thr Ala Val Ala Asp Asn Leu
2145                2150                2155                2160

ctc ttt tat ctt gga agt gcc aaa ttt att gac ttt ctg gct ata gaa   6528
Leu Phe Tyr Leu Gly Ser Ala Lys Phe Ile Asp Phe Leu Ala Ile Glu
               2165                2170                2175

atg cgt aaa ggc aaa gtc agc ttc ctc tgg gat gtt gga tct gga gtt   6576
Met Arg Lys Gly Lys Val Ser Phe Leu Trp Asp Val Gly Ser Gly Val
          2180                2185                2190

gga cgt gta gag tac cca gat ttg act att gat gac tca tat tgg tac   6624
Gly Arg Val Glu Tyr Pro Asp Leu Thr Ile Asp Asp Ser Tyr Trp Tyr
       2195                2200                2205

cgt atc gta gca tca aga act ggg aga aat gga act att tct gtg aga   6672
Arg Ile Val Ala Ser Arg Thr Gly Arg Asn Gly Thr Ile Ser Val Arg
   2210                2215                2220

gcc ctg gat gga ccc aaa gcc agc att gtg ccc agc aca cac cat tcg   6720
Ala Leu Asp Gly Pro Lys Ala Ser Ile Val Pro Ser Thr His His Ser
2225                2230                2235                2240

acg tct cct cca ggg tac acg att cta gat gtg gat gca aat gca atg   6768
Thr Ser Pro Pro Gly Tyr Thr Ile Leu Asp Val Asp Ala Asn Ala Met
               2245                2250                2255
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ctg ttt gtt ggt ggc ctg act ggg aaa tta aag aag gct gat gct gta   6816
Leu Phe Val Gly Gly Leu Thr Gly Lys Leu Lys Lys Ala Asp Ala Val
          2260                2265                2270

cgt gtg att aca ttc act ggc tgc atg gga gaa aca tac ttt gac aac   6864
Arg Val Ile Thr Phe Thr Gly Cys Met Gly Glu Thr Tyr Phe Asp Asn
       2275                2280                2285

aaa cct ata ggt ttg tgg aat ttc cga gaa aaa gaa ggt gac tgc aaa   6912
Lys Pro Ile Gly Leu Trp Asn Phe Arg Glu Lys Glu Gly Asp Cys Lys
   2290                2295                2300

gga tgc act gtc agt cct cag gtg gaa gat agt gag ggg act att caa   6960
Gly Cys Thr Val Ser Pro Gln Val Glu Asp Ser Glu Gly Thr Ile Gln
2305                2310                2315                2320

ttt gat gga gaa ggt tat gca ttg gtc agc cgt ccc att cgc tgg tac   7008
Phe Asp Gly Glu Gly Tyr Ala Leu Val Ser Arg Pro Ile Arg Trp Tyr
               2325                2330                2335

ccc aac atc tcc act gtc atg ttc aag ttc aga aca ttt tct tcg agt   7056
Pro Asn Ile Ser Thr Val Met Phe Lys Phe Arg Thr Phe Ser Ser Ser
          2340                2345                2350

gct ctt ctg atg tat ctt gcc aca cga gac ctg aga gat ttc atg agt   7104
Ala Leu Leu Met Tyr Leu Ala Thr Arg Asp Leu Arg Asp Phe Met Ser
       2355                2360                2365

gtg gag ctc act gat ggg cac ata aaa gtc agt tac gat ctg ggc tca   7152
Val Glu Leu Thr Asp Gly His Ile Lys Val Ser Tyr Asp Leu Gly Ser
   2370                2375                2380

gga atg gct tcc gtt gtc agc aat caa aac cat aat gat ggg aaa tgg   7200
Gly Met Ala Ser Val Val Ser Asn Gln Asn His Asn Asp Gly Lys Trp
2385                2390                2395                2400

aaa tca ttc act ctg tca aga att caa aaa caa gcc aat ata tca att   7248
Lys Ser Phe Thr Leu Ser Arg Ile Gln Lys Gln Ala Asn Ile Ser Ile
               2405                2410                2415

gta gat ata gat act aat cag gag gag aat ata gca act tcg tct tct   7296
Val Asp Ile Asp Thr Asn Gln Glu Glu Asn Ile Ala Thr Ser Ser Ser
          2420                2425                2430

gga aac aac ttt ggt ctt gac ttg aaa gca gat gac aaa ata tat ttt   7344
Gly Asn Asn Phe Gly Leu Asp Leu Lys Ala Asp Asp Lys Ile Tyr Phe
       2435                2440                2445

ggt ggc ctg cca acg ctg aga aac ttg agt atg aaa gca agg cca gaa   7392
Gly Gly Leu Pro Thr Leu Arg Asn Leu Ser Met Lys Ala Arg Pro Glu
   2450                2455                2460

gta aat ctg aag aaa tat tcc ggc tgc ctc aaa gat att gaa att tca   7440
Val Asn Leu Lys Lys Tyr Ser Gly Cys Leu Lys Asp Ile Glu Ile Ser
2465                2470                2475                2480

aga act ccg tac aat ata ctc agt agt ccc gat tat gtt ggt gtt acc   7488
Arg Thr Pro Tyr Asn Ile Leu Ser Ser Pro Asp Tyr Val Gly Val Thr
               2485                2490                2495

aaa gga tgt tcc ctg gag aat gtt tac aca gtt agc ttt cct aag cct   7536
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Lys Gly Cys Ser Leu Glu Asn Val Tyr Thr Val Ser Phe Pro Lys Pro
          2500                2505                2510

ggt ttt gtg gag ctc tcc cct gtg cca att gat gta gga aca gaa atc   7584
Gly Phe Val Glu Leu Ser Pro Val Pro Ile Asp Val Gly Thr Glu Ile
       2515                2520                2525

aac ctg tca ttc agc acc aag aat gag tcc ggc atc att ctt ttg gga   7632
Asn Leu Ser Phe Ser Thr Lys Asn Glu Ser Gly Ile Ile Leu Leu Gly
   2530                2535                2540

agt gga ggg aca cca gca cca cct agg aga aaa cga agg cag act gga   7680
Ser Gly Gly Thr Pro Ala Pro Pro Arg Arg Lys Arg Arg Gln Thr Gly
2545                2550                2555                2560

cag gcc tat tat gta ata ctc ctc aac agg ggc cgt ctg gaa gtg cat   7728
Gln Ala Tyr Tyr Val Ile Leu Leu Asn Arg Gly Arg Leu Glu Val His
               2565                2570                2575

ctc tcc aca ggg gca cga aca atg agg aaa att gtc atc aga cca gag   7776
Leu Ser Thr Gly Ala Arg Thr Met Arg Lys Ile Val Ile Arg Pro Glu
          2580                2585                2590

ccg aat ctg ttt cat gat gga aga gaa cat tcc gtt cat gta gag cga   7824
Pro Asn Leu Phe His Asp Gly Arg Glu His Ser Val His Val Glu Arg
       2595                2600                2605

act aga ggc atc ttt aca gtt caa gtg gat gaa aac aga aga tac atg   7872
Thr Arg Gly Ile Phe Thr Val Gln Val Asp Glu Asn Arg Arg Tyr Met
   2610                2615                2620

caa aac ctg aca gtt gaa cag cct atc gaa gtt aaa aag ctt ttc gtt   7920
Gln Asn Leu Thr Val Glu Gln Pro Ile Glu Val Lys Lys Leu Phe Val
2625                2630                2635                2640

ggg ggt gct cca cct gaa ttt caa cct tcc cca ctc aga aat att cct   7968
Gly Gly Ala Pro Pro Glu Phe Gln Pro Ser Pro Leu Arg Asn Ile Pro
               2645                2650                2655

cct ttt gaa ggc tgc ata tgg aat ctt gtt att aac tct gtc ccc atg   8016
Pro Phe Glu Gly Cys Ile Trp Asn Leu Val Ile Asn Ser Val Pro Met
          2660                2665                2670

gac ttt gca agg cct gtg tcc ttc aaa aat gct gac att ggt cgc tgt   8064
Asp Phe Ala Arg Pro Val Ser Phe Lys Asn Ala Asp Ile Gly Arg Cys
       2675                2680                2685

gcc cat cag aaa ctc cgt gaa gat gaa gat gga gca gct cca gct gaa   8112
Ala His Gln Lys Leu Arg Glu Asp Glu Asp Gly Ala Ala Pro Ala Glu
   2690                2695                2700

ata gtt atc cag cct gag cca gtt ccc acc cca gcc ttt cct acg ccc   8160
Ile Val Ile Gln Pro Glu Pro Val Pro Thr Pro Ala Phe Pro Thr Pro
2705                2710                2715                2720

acc cca gtt ctg aca cat ggt cct tgt gct gca gaa tca gaa cca gct   8208
Thr Pro Val Leu Thr His Gly Pro Cys Ala Ala Glu Ser Glu Pro Ala
               2725                2730                2735

ctt ttg ata ggg agc aag cag ttc ggg ctt tca aga aac agt cac att   8256
Leu Leu Ile Gly Ser Lys Gln Phe Gly Leu Ser Arg Asn Ser His Ile
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          2740                2745                2750

gca att gca ttt gat gac acc aaa gtt aaa aac cgt ctc aca att gag   8304
Ala Ile Ala Phe Asp Asp Thr Lys Val Lys Asn Arg Leu Thr Ile Glu
       2755                2760                2765

ttg gaa gta aga acc gaa gct gaa tcc ggc ttg ctt ttt tac atg gct   8352
Leu Glu Val Arg Thr Glu Ala Glu Ser Gly Leu Leu Phe Tyr Met Ala
   2770                2775                2780

gcg atc aat cat gct gat ttt gca aca gtt cag ctg aga aat gga ttg   8400
Ala Ile Asn His Ala Asp Phe Ala Thr Val Gln Leu Arg Asn Gly Leu
2785                2790                2795                2800

ccc tac ttc agc tat gac ttg ggg agt ggg gac acc cac acc atg atc   8448
Pro Tyr Phe Ser Tyr Asp Leu Gly Ser Gly Asp Thr His Thr Met Ile
             2805                2810                2815

ccc acc aaa atc aat gat ggc cag tgg cac aag att aag ata atg aga   8496
Pro Thr Lys Ile Asn Asp Gly Gln Trp His Lys Ile Lys Ile Met Arg
          2820                2825                2830

agt aag caa gaa gga att ctt tat gta gat ggg gct tcc aac aga acc   8544
Ser Lys Gln Glu Gly Ile Leu Tyr Val Asp Gly Ala Ser Asn Arg Thr
       2835                2840                2845

atc agt ccc aaa aaa gcc gac atc ctg gat gtc gtg gga atg ctg tat   8592
Ile Ser Pro Lys Lys Ala Asp Ile Leu Asp Val Val Gly Met Leu Tyr
   2850                2855                2860

gtt ggt ggg tta ccc atc aac tac act acc cga aga att ggt cca gtg   8640
Val Gly Gly Leu Pro Ile Asn Tyr Thr Thr Arg Arg Ile Gly Pro Val
2865                2870                2875                2880

acc tat agc att gat ggc tgc gtc agg aat ctc cac atg gca gag gcc   8688
Thr Tyr Ser Ile Asp Gly Cys Val Arg Asn Leu His Met Ala Glu Ala
             2885                2890                2895

cct gcc gat ctg gaa caa ccc acc tcc agc ttc cat gtt ggg aca tgt   8736
Pro Ala Asp Leu Glu Gln Pro Thr Ser Ser Phe His Val Gly Thr Cys
          2900                2905                2910

ttt gca aat gct cag agg gga aca tat ttt gac gga acc ggt ttt gcc   8784
Phe Ala Asn Ala Gln Arg Gly Thr Tyr Phe Asp Gly Thr Gly Phe Ala
       2915                2920                2925

aaa gca gtt ggt gga ttc aaa gtg gga ttg gac ctt ctt gta gaa ttt   8832
Lys Ala Val Gly Gly Phe Lys Val Gly Leu Asp Leu Leu Val Glu Phe
   2930                2935                2940

gaa ttc gcg aca act aca acg act gga gtt ctt ctg ggg atc agt agt   8880
Glu Phe Ala Thr Thr Thr Thr Thr Gly Val Leu Leu Gly Ile Ser Ser
2945                2950                2955                2960

caa aaa atg gat gga atg ggt att gaa atg att gat gaa aag ttg atg   8928
Gln Lys Met Asp Gly Met Gly Ile Glu Met Ile Asp Glu Lys Leu Met
             2965                2970                2975

ttt cat gtg gac aat ggt gcg ggc aga ttc act gct gtc tat gat gct   8976
Phe His Val Asp Asn Gly Ala Gly Arg Phe Thr Ala Val Tyr Asp Ala
          2980                2985                2990
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ggg gtt cca ggg cat ttg tgt gat gga caa tgg cat aaa gtc act gcc   9024
Gly Val Pro Gly His Leu Cys Asp Gly Gln Trp His Lys Val Thr Ala
       2995                3000                3005

aac aag atc aaa cac cgc att gag ctc aca gtc gat ggg aac cag gtg   9072
Asn Lys Ile Lys His Arg Ile Glu Leu Thr Val Asp Gly Asn Gln Val
   3010                3015                3020

gaa gcc caa agc cca aac cca gca tct aca tca gct gac aca aat gac   9120
Glu Ala Gln Ser Pro Asn Pro Ala Ser Thr Ser Ala Asp Thr Asn Asp
3025                3030                3035                3040

cct gtg ttt gtt gga ggc ttc cca gat gac ctc aag cag ttt ggc cta   9168
Pro Val Phe Val Gly Gly Phe Pro Asp Asp Leu Lys Gln Phe Gly Leu
                3045                3050                3055

aca acc agt att ccg ttc cga ggt tgc atc aga tcc ctg aag ctc acc   9216
Thr Thr Ser Ile Pro Phe Arg Gly Cys Ile Arg Ser Leu Lys Leu Thr
            3060                3065                3070

aaa ggc aca gca agc cac tgg agg tta att ttg cca agg ccc tgg aac   9264
Lys Gly Thr Ala Ser His Trp Arg Leu Ile Leu Pro Arg Pro Trp Asn
       3075                3080                3085

tgaggggcgt tcaacctgta tcatgcccag ccaactaata aaaataagtg taaccccagg 9324

aagagtctgt caaaacaagt atatcaagta aaacaaacaa atatatttta cctatatatg 9384

ttaattaaac taatttgtgc atgtacatag aattc                           9419
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<210> 8
<211> 3088
<212> PRT
<213> Homo sapiens

<400> 8

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Gln Arg Pro Gln Gln Gln Arg Gln Ser Gln Ala His Gln Gln Arg Gly
  1               5                  10                  15

Leu Phe Pro Ala Val Leu Asn Leu Ala Ser Asn Ala Leu Ile Thr Thr
            20                  25                  30

Asn Ala Thr Cys Gly Glu Lys Gly Pro Glu Met Tyr Cys Lys Leu Val
        35                  40                  45

Glu His Val Pro Gly Gln Pro Val Arg Asn Pro Gln Cys Arg Ile Cys
    50                  55                  60

Asn Gln Asn Ser Ser Asn Pro Asn Gln Arg His Pro Ile Thr Asn Ala
65                  70                  75                  80

Ile Asp Gly Lys Asn Thr Trp Trp Gln Ser Pro Ser Ile Lys Asn Gly
                85                  90                  95

Ile Glu Tyr His Tyr Val Thr Ile Thr Leu Asp Leu Gln Gln Val Phe
            100                 105                 110

Gln Ile Ala Tyr Val Ile Val Lys Ala Ala Asn Ser Pro Arg Pro Gly
        115                 120                 125
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Asn Trp Ile Leu Glu Arg Ser Leu Asp Asp Val Glu Tyr Lys Pro Trp
    130                 135                 140

Gln Tyr His Ala Val Thr Asp Thr Glu Cys Leu Thr Leu Tyr Asn Ile
145                 150                 155                 160

Tyr Pro Arg Thr Gly Pro Pro Ser Tyr Ala Lys Asp Asp Glu Val Ile
                165                 170                 175

Cys Thr Ser Phe Tyr Ser Lys Ile His Pro Leu Glu Asn Gly Glu Ile
            180                 185                 190

His Ile Ser Leu Ile Asn Gly Arg Pro Ser Ala Asp Asp Pro Ser Pro
        195                 200                 205

Glu Leu Leu Glu Phe Thr Ser Ala Arg Tyr Ile Arg Leu Arg Phe Gln
    210                 215                 220

Arg Ile Arg Thr Leu Asn Ala Asp Leu Met Met Phe Ala His Lys Asp
225                 230                 235                 240

Pro Arg Glu Ile Asp Pro Ile Val Thr Arg Arg Tyr Tyr Tyr Ser Val
                245                 250                 255

Lys Asp Ile Ser Val Gly Gly Met Cys Ile Cys Tyr Gly His Ala Arg
            260                 265                 270

Ala Cys Pro Leu Asp Pro Ala Thr Asn Lys Ser Arg Cys Glu Cys Glu
        275                 280                 285

His Asn Thr Cys Gly Asp Ser Cys Asp Gln Cys Cys Pro Gly Phe His
    290                 295                 300

Gln Lys Pro Trp Arg Ala Gly Thr Phe Leu Thr Lys Thr Glu Cys Glu
305                 310                 315                 320

Ala Cys Asn Cys His Gly Lys Ala Glu Glu Cys Tyr Tyr Asp Glu Asn
                325                 330                 335

Val Ala Arg Arg Asn Leu Ser Leu Asn Ile Arg Gly Lys Tyr Ile Gly
            340                 345                 350

Gly Gly Val Cys Ile Asn Cys Thr Gln Asn Thr Ala Gly Ile Asn Cys
        355                 360                 365

Glu Thr Cys Thr Asp Gly Phe Phe Arg Pro Lys Gly Val Ser Pro Asn
    370                 375                 380

Tyr Pro Arg Pro Cys Gln Pro Cys His Cys Asp Pro Ile Gly Ser Leu
385                 390                 395                 400

Asn Glu Val Cys Val Lys Asp Glu Lys His Ala Arg Arg Gly Leu Ala
                405                 410                 415

Pro Gly Ser Cys His Cys Lys Thr Gly Phe Gly Gly Val Ser Cys Asp
            420                 425                 430

Arg Cys Ala Arg Gly Tyr Thr Gly Tyr Pro Asp Cys Lys Ala Cys Asn
        435                 440                 445
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Cys Ser Gly Leu Gly Ser Lys Asn Glu Asp Pro Cys Phe Gly Pro Cys
    450                 455                 460

Ile Cys Lys Glu Asn Val Glu Gly Gly Asp Cys Ser Arg Cys Lys Ser
465                 470                 475                 480

Gly Phe Phe Asn Leu Gln Glu Asp Asn Trp Lys Gly Cys Asp Glu Cys
                485                 490                 495

Phe Cys Ser Gly Val Ser Asn Arg Cys Gln Ser Ser Tyr Trp Thr Tyr
            500                 505                 510

Gly Lys Ile Gln Asp Met Ser Gly Trp Tyr Leu Thr Asp Leu Pro Gly
        515                 520                 525

Arg Ile Arg Val Ala Pro Gln Gln Asp Asp Leu Asp Ser Pro Gln Gln
    530                 535                 540

Ile Ser Ile Ser Asn Ala Glu Ala Arg Gln Ala Leu Pro His Ser Tyr
545                 550                 555                 560

Tyr Trp Ser Ala Pro Ala Pro Tyr Leu Gly Asn Lys Leu Pro Ala Val
                565                 570                 575

Gly Gly Gln Leu Thr Phe Thr Ile Ser Tyr Asp Leu Glu Glu Glu Glu
            580                 585                 590

Glu Asp Thr Glu Arg Val Leu Gln Leu Met Ile Ile Leu Glu Gly Asn
        595                 600                 605

Asp Leu Ser Ile Ser Thr Ala Gln Asp Glu Val Tyr Leu His Pro Ser
    610                 615                 620

Glu Glu His Thr Asn Val Leu Leu Leu Lys Glu Glu Ser Phe Thr Ile
625                 630                 635                 640

His Gly Thr His Phe Pro Val Arg Arg Lys Glu Phe Met Thr Val Leu
                645                 650                 655

Ala Asn Leu Lys Arg Val Leu Leu Gln Ile Thr Tyr Ser Phe Gly Met
            660                 665                 670

Asp Ala Ile Phe Arg Leu Ser Ser Val Asn Leu Glu Ser Ala Val Ser
        675                 680                 685

Tyr Pro Thr Asp Gly Ser Ile Ala Ala Ala Val Glu Val Cys Gln Cys
    690                 695                 700

Pro Pro Gly Tyr Thr Gly Ser Ser Cys Glu Ser Cys Trp Pro Arg His
705                 710                 715                 720

Arg Arg Val Asn Gly Thr Ile Phe Gly Gly Ile Cys Glu Pro Cys Gln
                725                 730                 735

Cys Phe Gly His Ala Glu Ser Cys Asp Asp Val Thr Gly Glu Cys Leu
            740                 745                 750

Asn Cys Lys Asp His Thr Gly Gly Pro Tyr Cys Asp Lys Cys Leu Pro
        755                 760                 765

Gly Phe Tyr Gly Glu Pro Thr Lys Gly Thr Ser Glu Asp Cys Gln Pro
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    770                 775                 780

Cys Ala Cys Pro Leu Asn Ile Pro Ser Asn Asn Phe Ser Pro Thr Cys
785                 790                 795                 800

His Leu Asp Arg Ser Leu Gly Leu Ile Cys Asp Gly Cys Pro Val Gly
                805                 810                 815

Tyr Thr Gly Pro Arg Cys Glu Arg Cys Ala Glu Gly Tyr Phe Gly Gln
            820                 825                 830

Pro Ser Val Pro Gly Gly Ser Cys Gln Pro Cys Gln Cys Asn Asp Asn
        835                 840                 845

Leu Asp Phe Ser Ile Pro Gly Ser Cys Asp Ser Leu Ser Gly Ser Cys
    850                 855                 860

Leu Ile Cys Lys Pro Gly Thr Thr Gly Arg Tyr Cys Glu Leu Cys Ala
865                 870                 875                 880

Asp Gly Tyr Phe Gly Asp Ala Val Asp Ala Lys Asn Cys Gln Pro Cys
                885                 890                 895

Arg Cys Asn Ala Gly Gly Ser Phe Ser Glu Val Cys His Ser Gln Thr
            900                 905                 910

Gly Gln Cys Glu Cys Arg Ala Asn Val Gln Gly Gln Arg Cys Asp Lys
        915                 920                 925

Cys Lys Ala Gly Thr Phe Gly Leu Gln Ser Ala Arg Gly Cys Val Pro
    930                 935                 940

Cys Asn Cys Asn Ser Phe Gly Ser Lys Ser Phe Asp Cys Glu Glu Ser
945                 950                 955                 960

Gly Gln Cys Trp Cys Gln Pro Gly Val Thr Gly Lys Lys Cys Asp Arg
                965                 970                 975

Cys Ala His Gly Tyr Phe Asn Phe Gln Glu Gly Gly Cys Thr Ala Cys
            980                 985                 990

Glu Cys Ser His Leu Gly Asn Asn Cys Asp Pro Lys Thr Gly Arg Cys
        995                1000                1005

Ile Cys Pro Pro Asn Thr Ile Gly Glu Lys Cys Ser Lys Cys Ala Pro
   1010                1015                1020

Asn Thr Trp Gly His Ser Ile Thr Thr Gly Cys Lys Ala Cys Asn Cys
1025                1030                1035                1040

Ser Thr Val Gly Ser Leu Asp Phe Gln Cys Asn Val Asn Thr Gly Gln
                1045                1050                1055

Cys Asn Cys His Pro Lys Phe Ser Gly Ala Lys Cys Thr Glu Cys Ser
            1060                1065                1070

Arg Gly His Trp Asn Tyr Pro Arg Cys Asn Leu Cys Asp Cys Phe Leu
        1075                1080                1085

Pro Gly Thr Asp Ala Thr Thr Cys Asp Ser Glu Thr Lys Lys Cys Ser
   1090                1095                1100
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Cys Ser Asp Gln Thr Gly Gln Cys Thr Cys Lys Val Asn Val Glu Gly
1105                1110                1115                1120

Ile His Cys Asp Arg Cys Arg Pro Gly Lys Phe Gly Leu Asp Ala Lys
                1125                1130                1135

Asn Pro Leu Gly Cys Ser Ser Cys Tyr Cys Phe Gly Thr Thr Thr Gln
            1140                1145                1150

Cys Ser Glu Ala Lys Gly Leu Ile Arg Thr Trp Val Thr Leu Lys Ala
        1155                1160                1165

Glu Gln Thr Ile Leu Pro Leu Val Asp Glu Ala Leu Gln His Thr Thr
    1170                1175                1180

Thr Lys Gly Ile Val Phe Gln His Pro Glu Ile Val Ala His Met Asp
1185                1190                1195                1200

Leu Met Arg Glu Asp Leu His Leu Glu Pro Phe Tyr Trp Lys Leu Pro
                1205                1210                1215

Glu Gln Phe Glu Gly Lys Lys Leu Met Ala Tyr Gly Gly Lys Leu Lys
            1220                1225                1230

Tyr Ala Ile Tyr Phe Glu Ala Arg Glu Glu Thr Gly Phe Ser Thr Tyr
        1235                1240                1245

Asn Pro Gln Val Ile Ile Arg Gly Gly Thr Pro Thr His Ala Arg Ile
    1250                1255                1260

Ile Val Arg His Met Ala Ala Pro Leu Ile Gly Gln Leu Thr Arg His
1265                1270                1275                1280

Glu Ile Glu Met Thr Glu Lys Glu Trp Lys Tyr Tyr Gly Asp Asp Pro
                1285                1290                1295

Arg Val His Arg Thr Val Thr Arg Glu Asp Phe Leu Asp Ile Leu Tyr
            1300                1305                1310

Asp Ile His Tyr Ile Leu Ile Lys Ala Thr Tyr Gly Asn Phe Met Arg
        1315                1320                1325

Gln Ser Arg Ile Ser Glu Ile Ser Met Glu Val Ala Glu Gln Gly Arg
    1330                1335                1340

Gly Thr Thr Met Thr Pro Pro Ala Asp Leu Ile Glu Lys Cys Asp Cys
1345                1350                1355                1360

Pro Leu Gly Tyr Ser Gly Leu Ser Cys Glu Ala Cys Leu Pro Gly Phe
                1365                1370                1375

Tyr Arg Leu Arg Ser Gln Pro Gly Gly Arg Thr Pro Gly Pro Thr Leu
            1380                1385                1390

Gly Thr Cys Val Pro Cys Gln Cys Asn Gly His Ser Ser Leu Cys Asp
        1395                1400                1405

Pro Glu Thr Ser Ile Cys Gln Asn Cys Gln His His Thr Ala Gly Asp
    1410                1415                1420
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Phe Cys Glu Arg Cys Ala Leu Gly Tyr Tyr Gly Ile Val Lys Gly Leu
1425                1430                1435                1440

Pro Asn Asp Cys Gln Gln Cys Ala Cys Pro Leu Ile Ser Ser Ser Asn
                1445                1450                1455

Asn Phe Ser Pro Ser Cys Val Ala Glu Gly Leu Asp Asp Tyr Arg Cys
            1460                1465                1470

Thr Ala Cys Pro Arg Gly Tyr Glu Gly Gln Tyr Cys Glu Arg Cys Ala
        1475                1480                1485

Pro Gly Tyr Thr Gly Ser Pro Gly Asn Pro Gly Gly Ser Cys Gln Glu
    1490                1495                1500

Cys Glu Cys Asp Pro Tyr Gly Ser Leu Pro Val Pro Cys Asp Pro Val
1505                1510                1515                1520

Thr Gly Phe Cys Thr Cys Arg Pro Gly Ala Thr Gly Arg Lys Cys Asp
                1525                1530                1535

Gly Cys Lys His Trp His Ala Arg Glu Gly Trp Glu Cys Val Phe Cys
            1540                1545                1550

Gly Asp Glu Cys Thr Gly Leu Leu Leu Gly Asp Leu Ala Arg Leu Glu
        1555                1560                1565

Gln Met Val Met Ser Ile Asn Leu Thr Gly Pro Leu Pro Ala Pro Tyr
    1570                1575                1580

Lys Met Leu Tyr Gly Leu Glu Asn Met Thr Gln Glu Leu Lys His Leu
1585                1590                1595                1600

Leu Ser Pro Gln Arg Ala Pro Glu Arg Leu Ile Gln Leu Ala Glu Gly
                1605                1610                1615

Asn Leu Asn Thr Leu Val Thr Glu Met Asn Glu Leu Leu Thr Arg Ala
            1620                1625                1630

Thr Lys Val Thr Ala Asp Gly Glu Gln Thr Gly Gln Asp Ala Glu Arg
        1635                1640                1645

Thr Asn Thr Arg Ala Lys Ser Leu Gly Glu Phe Ile Lys Glu Leu Ala
    1650                1655                1660

Arg Asp Ala Glu Ala Val Asn Glu Lys Ala Ile Lys Leu Asn Glu Thr
1665                1670                1675                1680

Leu Gly Thr Arg Asp Glu Ala Phe Glu Arg Asn Leu Glu Gly Leu Gln
                1685                1690                1695

Lys Glu Ile Asp Gln Met Ile Lys Glu Leu Arg Arg Lys Asn Leu Glu
            1700                1705                1710

Thr Gln Lys Glu Ile Ala Glu Asp Glu Leu Val Ala Ala Glu Ala Leu
        1715                1720                1725

Leu Lys Lys Val Lys Lys Leu Phe Gly Glu Ser Arg Gly Glu Asn Glu
    1730                1735                1740

Glu Met Glu Lys Asp Leu Arg Glu Lys Leu Ala Asp Tyr Lys Asn Lys
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1745                1750                1755                1760

Val Asp Asp Ala Trp Asp Leu Leu Arg Glu Ala Thr Asp Lys Ile Arg
                1765                1770                1775

Glu Ala Asn Arg Leu Phe Ala Val Asn Gln Lys Asn Met Thr Ala Leu
            1780                1785                1790

Glu Lys Lys Lys Glu Ala Val Glu Ser Gly Lys Arg Gln Ile Glu Asn
        1795                1800                1805

Thr Leu Lys Glu Gly Asn Asp Ile Leu Asp Glu Ala Asn Arg Leu Ala
    1810                1815                1820

Asp Glu Ile Asn Ser Ile Ile Asp Tyr Val Glu Asp Ile Gln Thr Lys
1825                1830                1835                1840

Leu Pro Pro Met Ser Glu Glu Leu Asn Asp Lys Ile Asp Asp Leu Ser
                1845                1850                1855

Gln Glu Ile Lys Asp Arg Lys Leu Ala Glu Lys Val Ser Gln Ala Glu
            1860                1865                1870

Ser His Ala Ala Gln Leu Asn Asp Ser Ser Ala Val Leu Asp Gly Ile
        1875                1880                1885

Leu Asp Glu Ala Lys Asn Ile Ser Phe Asn Ala Thr Ala Ala Phe Lys
    1890                1895                1900

Ala Tyr Ser Asn Ile Lys Asp Tyr Ile Asp Glu Ala Glu Lys Val Ala
1905                1910                1915                1920

Lys Glu Ala Lys Asp Leu Ala His Glu Ala Thr Lys Leu Ala Thr Gly
                1925                1930                1935

Pro Arg Gly Leu Leu Lys Glu Asp Ala Lys Gly Cys Leu Gln Lys Ser
            1940                1945                1950

Phe Arg Ile Leu Asn Glu Ala Lys Lys Leu Ala Asn Asp Val Lys Glu
        1955                1960                1965

Asn Glu Asp His Leu Asn Gly Leu Lys Thr Arg Ile Glu Asn Ala Asp
    1970                1975                1980

Ala Arg Asn Gly Asp Leu Leu Arg Thr Leu Asn Asp Thr Leu Gly Lys
1985                1990                1995                2000

Leu Ser Ala Ile Pro Asn Asp Thr Ala Ala Lys Leu Gln Ala Val Lys
                2005                2010                2015

Asp Lys Ala Arg Gln Ala Asn Asp Thr Ala Lys Asp Val Leu Ala Gln
            2020                2025                2030

Ile Thr Glu Leu His Gln Asn Leu Asp Gly Leu Lys Lys Asn Tyr Asn
        2035                2040                2045

Lys Leu Ala Asp Ser Val Ala Lys Thr Asn Ala Val Val Lys Asp Pro
    2050                2055                2060

Ser Lys Asn Lys Ile Ile Ala Asp Ala Asp Ala Thr Val Lys Asn Leu
2065                2070                2075                2080
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Glu Gln Glu Ala Asp Arg Leu Ile Asp Lys Leu Lys Pro Ile Lys Glu
              2085                2090                2095

Leu Glu Asp Asn Leu Lys Lys Asn Ile Ser Glu Ile Lys Glu Leu Ile
          2100                2105                2110

Asn Gln Ala Arg Lys Gln Ala Asn Ser Ile Lys Val Ser Val Ser Ser
       2115                2120                2125

Gly Gly Asp Cys Ile Arg Thr Tyr Lys Pro Glu Ile Lys Lys Gly Ser
   2130                2135                2140

Tyr Asn Asn Ile Val Val Asn Val Lys Thr Ala Val Ala Asp Asn Leu
2145                2150                2155                2160

Leu Phe Tyr Leu Gly Ser Ala Lys Phe Ile Asp Phe Leu Ala Ile Glu
              2165                2170                2175

Met Arg Lys Gly Lys Val Ser Phe Leu Trp Asp Val Gly Ser Gly Val
          2180                2185                2190

Gly Arg Val Glu Tyr Pro Asp Leu Thr Ile Asp Asp Ser Tyr Trp Tyr
       2195                2200                2205

Arg Ile Val Ala Ser Arg Thr Gly Arg Asn Gly Thr Ile Ser Val Arg
   2210                2215                2220

Ala Leu Asp Gly Pro Lys Ala Ser Ile Val Pro Ser Thr His His Ser
2225                2230                2235                2240

Thr Ser Pro Pro Gly Tyr Thr Ile Leu Asp Val Asp Ala Asn Ala Met
              2245                2250                2255

Leu Phe Val Gly Gly Leu Thr Gly Lys Leu Lys Lys Ala Asp Ala Val
          2260                2265                2270

Arg Val Ile Thr Phe Thr Gly Cys Met Gly Glu Thr Tyr Phe Asp Asn
       2275                2280                2285

Lys Pro Ile Gly Leu Trp Asn Phe Arg Glu Lys Glu Gly Asp Cys Lys
   2290                2295                2300

Gly Cys Thr Val Ser Pro Gln Val Glu Asp Ser Glu Gly Thr Ile Gln
2305                2310                2315                2320

Phe Asp Gly Glu Gly Tyr Ala Leu Val Ser Arg Pro Ile Arg Trp Tyr
              2325                2330                2335

Pro Asn Ile Ser Thr Val Met Phe Lys Phe Arg Thr Phe Ser Ser Ser
          2340                2345                2350

Ala Leu Leu Met Tyr Leu Ala Thr Arg Asp Leu Arg Asp Phe Met Ser
       2355                2360                2365

Val Glu Leu Thr Asp Gly His Ile Lys Val Ser Tyr Asp Leu Gly Ser
   2370                2375                2380

Gly Met Ala Ser Val Val Ser Asn Gln Asn His Asn Asp Gly Lys Trp
2385                2390                2395                2400
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Lys Ser Phe Thr Leu Ser Arg Ile Gln Lys Gln Ala Asn Ile Ser Ile
                2405                2410                2415

Val Asp Ile Asp Thr Asn Gln Glu Glu Asn Ile Ala Thr Ser Ser Ser
            2420                2425                2430

Gly Asn Asn Phe Gly Leu Asp Leu Lys Ala Asp Asp Lys Ile Tyr Phe
        2435                2440                2445

Gly Gly Leu Pro Thr Leu Arg Asn Leu Ser Met Lys Ala Arg Pro Glu
    2450                2455                2460

Val Asn Leu Lys Lys Tyr Ser Gly Cys Leu Lys Asp Ile Glu Ile Ser
2465                2470                2475                2480

Arg Thr Pro Tyr Asn Ile Leu Ser Ser Pro Asp Tyr Val Gly Val Thr
                2485                2490                2495

Lys Gly Cys Ser Leu Glu Asn Val Tyr Thr Val Ser Phe Pro Lys Pro
            2500                2505                2510

Gly Phe Val Glu Leu Ser Pro Val Pro Ile Asp Val Gly Thr Glu Ile
        2515                2520                2525

Asn Leu Ser Phe Ser Thr Lys Asn Glu Ser Gly Ile Ile Leu Leu Gly
    2530                2535                2540

Ser Gly Gly Thr Pro Ala Pro Pro Arg Arg Lys Arg Arg Gln Thr Gly
2545                2550                2555                2560

Gln Ala Tyr Tyr Val Ile Leu Leu Asn Arg Gly Arg Leu Glu Val His
                2565                2570                2575

Leu Ser Thr Gly Ala Arg Thr Met Arg Lys Ile Val Ile Arg Pro Glu
            2580                2585                2590

Pro Asn Leu Phe His Asp Gly Arg Glu His Ser Val His Val Glu Arg
        2595                2600                2605

Thr Arg Gly Ile Phe Thr Val Gln Val Asp Glu Asn Arg Arg Tyr Met
    2610                2615                2620

Gln Asn Leu Thr Val Glu Gln Pro Ile Glu Val Lys Lys Leu Phe Val
2625                2630                2635                2640

Gly Gly Ala Pro Pro Glu Phe Gln Pro Ser Pro Leu Arg Asn Ile Pro
                2645                2650                2655

Pro Phe Glu Gly Cys Ile Trp Asn Leu Val Ile Asn Ser Val Pro Met
            2660                2665                2670

Asp Phe Ala Arg Pro Val Ser Phe Lys Asn Ala Asp Ile Gly Arg Cys
        2675                2680                2685

Ala His Gln Lys Leu Arg Glu Asp Glu Asp Gly Ala Ala Pro Ala Glu
    2690                2695                2700

Ile Val Ile Gln Pro Glu Pro Val Pro Thr Pro Ala Phe Pro Thr Pro
2705                2710                2715                2720

Thr Pro Val Leu Thr His Gly Pro Cys Ala Ala Glu Ser Glu Pro Ala
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                2725                2730                2735

Leu Leu Ile Gly Ser Lys Gln Phe Gly Leu Ser Arg Asn Ser His Ile
            2740                2745                2750

Ala Ile Ala Phe Asp Asp Thr Lys Val Lys Asn Arg Leu Thr Ile Glu
        2755                2760                2765

Leu Glu Val Arg Thr Glu Ala Glu Ser Gly Leu Leu Phe Tyr Met Ala
    2770                2775                2780

Ala Ile Asn His Ala Asp Phe Ala Thr Val Gln Leu Arg Asn Gly Leu
2785                2790                2795                2800

Pro Tyr Phe Ser Tyr Asp Leu Gly Ser Gly Asp Thr His Thr Met Ile
                2805                2810                2815

Pro Thr Lys Ile Asn Asp Gly Gln Trp His Lys Ile Lys Ile Met Arg
            2820                2825                2830

Ser Lys Gln Glu Gly Ile Leu Tyr Val Asp Gly Ala Ser Asn Arg Thr
        2835                2840                2845

Ile Ser Pro Lys Lys Ala Asp Ile Leu Asp Val Val Gly Met Leu Tyr
    2850                2855                2860

Val Gly Gly Leu Pro Ile Asn Tyr Thr Thr Arg Arg Ile Gly Pro Val
2865                2870                2875                2880

Thr Tyr Ser Ile Asp Gly Cys Val Arg Asn Leu His Met Ala Glu Ala
                2885                2890                2895

Pro Ala Asp Leu Glu Gln Pro Thr Ser Ser Phe His Val Gly Thr Cys
            2900                2905                2910

Phe Ala Asn Ala Gln Arg Gly Thr Tyr Phe Asp Gly Thr Gly Phe Ala
        2915                2920                2925

Lys Ala Val Gly Gly Phe Lys Val Gly Leu Asp Leu Leu Val Glu Phe
    2930                2935                2940

Glu Phe Ala Thr Thr Thr Thr Thr Gly Val Leu Leu Gly Ile Ser Ser
2945                2950                2955                2960

Gln Lys Met Asp Gly Met Gly Ile Glu Met Ile Asp Glu Lys Leu Met
                2965                2970                2975

Phe His Val Asp Asn Gly Ala Gly Arg Phe Thr Ala Val Tyr Asp Ala
            2980                2985                2990

Gly Val Pro Gly His Leu Cys Asp Gly Gln Trp His Lys Val Thr Ala
        2995                3000                3005

Asn Lys Ile Lys His Arg Ile Glu Leu Thr Val Asp Gly Asn Gln Val
    3010                3015                3020

Glu Ala Gln Ser Pro Asn Pro Ala Ser Thr Ser Ala Asp Thr Asn Asp
3025                3030                3035                3040

Pro Val Phe Val Gly Gly Phe Pro Asp Asp Leu Lys Gln Phe Gly Leu
                3045                3050                3055
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Thr Thr Ser Ile Pro Phe Arg Gly Cys Ile Arg Ser Leu Lys Leu Thr
          3060                3065                3070

Lys Gly Thr Ala Ser His Trp Arg Leu Ile Leu Pro Arg Pro Trp Asn
       3075                3080                3085


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Pro Ala Ala Thr Ala Gly Ile Leu Leu Leu Leu Leu Leu Gly Thr Leu
             5                  10                  15

gaa ggc tcc cag act cag cgg cga cag tcc caa gcg cat caa cag aga   153
Glu Gly Ser Gln Thr Gln Arg Arg Gln Ser Gln Ala His Gln Gln Arg
         20                  25                  30

ggt tta ttt cct gct gtc ctg aat ctt gct tcg aat gca ctc atc aca   201
Gly Leu Phe Pro Ala Val Leu Asn Leu Ala Ser Asn Ala Leu Ile Thr
     35                  40                  45

acc aat gct aca tgt ggg gaa aaa gga ccc gag atg tac tgc aag ttg   249
Thr Asn Ala Thr Cys Gly Glu Lys Gly Pro Glu Met Tyr Cys Lys Leu
 50                  55                  60                  65

gtg gaa cat gtc ccc ggg cag cct gtg agg aac cct cag tgc cga atc   297
Val Glu His Val Pro Gly Gln Pro Val Arg Asn Pro Gln Cys Arg Ile
                 70                  75                  80

tgc aat cag aac agc agc aat cca tac cag agg cac ccg att acg aat   345
Cys Asn Gln Asn Ser Ser Asn Pro Tyr Gln Arg His Pro Ile Thr Asn
             85                  90                  95

gct att gat ggc aag aac aca tgg tgg cag agt ccc agt atc aag aat   393
Ala Ile Asp Gly Lys Asn Thr Trp Trp Gln Ser Pro Ser Ile Lys Asn
        100                 105                 110

gga gtg gaa tac cat tat gtg aca att act ctg gat tta cag cag gtg   441
Gly Val Glu Tyr His Tyr Val Thr Ile Thr Leu Asp Leu Gln Gln Val
    115                 120                 125

ttc cag att gcc tac gta att gtg aag gca gcc aat tcc cct cgg cct   489
Phe Gln Ile Ala Tyr Val Ile Val Lys Ala Ala Asn Ser Pro Arg Pro
130                 135                 140                 145
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gga aac tgg att ttg gaa cgt tcc ctg gat gac gtg gag tac aaa ccc   537
Gly Asn Trp Ile Leu Glu Arg Ser Leu Asp Asp Val Glu Tyr Lys Pro
                150                 155                 160

tgg cag tat cat gcg gtg aca gac acg gag tgc ctg acc ctc tac aat   585
Trp Gln Tyr His Ala Val Thr Asp Thr Glu Cys Leu Thr Leu Tyr Asn
            165                 170                 175

atc tat ccc cgc act gga cca cca tcc tac gcc aaa gat gat gag gtc   633
Ile Tyr Pro Arg Thr Gly Pro Pro Ser Tyr Ala Lys Asp Asp Glu Val
        180                 185                 190

atc tgc act tca ttt tat tcg aag atc cac cct tta gaa aat gga gag   681
Ile Cys Thr Ser Phe Tyr Ser Lys Ile His Pro Leu Glu Asn Gly Glu
    195                 200                 205

att cac att tct ttg atc aat ggg aga cca agt gct gat gac ccc tcc   729
Ile His Ile Ser Leu Ile Asn Gly Arg Pro Ser Ala Asp Asp Pro Ser
210                 215                 220                 225

cct gaa ctc ctg gaa ttc acc tct gct cgc tac att cgc ctg aga ttt   777
Pro Glu Leu Leu Glu Phe Thr Ser Ala Arg Tyr Ile Arg Leu Arg Phe
                230                 235                 240

cag agg atc cgc acc ttg aat gca gac ttg atg atg ttt gct cac aaa   825
Gln Arg Ile Arg Thr Leu Asn Ala Asp Leu Met Met Phe Ala His Lys
            245                 250                 255

gac ccc aga gaa atc gat ccc att gtc aca cga aga tat tac tat tct   873
Asp Pro Arg Glu Ile Asp Pro Ile Val Thr Arg Arg Tyr Tyr Tyr Ser
        260                 265                 270

gtc aag gat att tca gtt ggc ggg atg tgc atc tgt tat ggt cat gcc   921
Val Lys Asp Ile Ser Val Gly Gly Met Cys Ile Cys Tyr Gly His Ala
    275                 280                 285

cgg gct tgt cca ctt gac cct gca aca aat aaa tca cgc tgt gag tgt   969
Arg Ala Cys Pro Leu Asp Pro Ala Thr Asn Lys Ser Arg Cys Glu Cys
290                 295                 300                 305

gaa cat aac acc tgt ggg gaa agc tgt gac agg tgc tgt cca gga ttc  1017
Glu His Asn Thr Cys Gly Glu Ser Cys Asp Arg Cys Cys Pro Gly Phe
                310                 315                 320

cat cag aag cct tgg aga gct gga acc ttc ctc acc aag tct gag tgt  1065
His Gln Lys Pro Trp Arg Ala Gly Thr Phe Leu Thr Lys Ser Glu Cys
            325                 330                 335

gaa gca tgc aat tgt cac gga aaa gct gag gaa tgc tat tat gat gaa  1113
Glu Ala Cys Asn Cys His Gly Lys Ala Glu Glu Cys Tyr Tyr Asp Glu
        340                 345                 350

act gtt gct agc aga aat cta agt tta aat ata cat ggg aag tac atc  1161
Thr Val Ala Ser Arg Asn Leu Ser Leu Asn Ile His Gly Lys Tyr Ile
    355                 360                 365

gga ggg ggt gtg tgc atc aac tgc aca cat aac acg gct ggg ata aat  1209
Gly Gly Gly Val Cys Ile Asn Cys Thr His Asn Thr Ala Gly Ile Asn
370                 375                 380                 385
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tgt gag aca tgt gtt gat gga ttc ttc aga ccc aaa ggg gtg tca cca   1257
Cys Glu Thr Cys Val Asp Gly Phe Phe Arg Pro Lys Gly Val Ser Pro
               390                 395                 400

aat tat cca aga cca tgc cag cca tgt cac tgt gat cca act ggc tcc   1305
Asn Tyr Pro Arg Pro Cys Gln Pro Cys His Cys Asp Pro Thr Gly Ser
           405                 410                 415

ctt agt gaa gtc tgt gtc aaa gat gag aaa tac gcc cag cga ggg ttg   1353
Leu Ser Glu Val Cys Val Lys Asp Glu Lys Tyr Ala Gln Arg Gly Leu
       420                 425                 430

aaa cct gga tcc tgt cac tgc aaa act ggc ttt gga ggc gtg aac tgt   1401
Lys Pro Gly Ser Cys His Cys Lys Thr Gly Phe Gly Gly Val Asn Cys
   435                 440                 445

gat cgc tgt gtc agg ggt tac cat ggt tac cca gac tgc caa ccc tgt   1449
Asp Arg Cys Val Arg Gly Tyr His Gly Tyr Pro Asp Cys Gln Pro Cys
450                 455                 460                 465

aac tgt agt ggc ttg ggg agc aca aat gag gac cct tgc gtt ggg ccc   1497
Asn Cys Ser Gly Leu Gly Ser Thr Asn Glu Asp Pro Cys Val Gly Pro
               470                 475                 480

tgt agc tgt aag gag aat gtt gaa ggt gaa gac tgt agt cgt tgc aaa   1545
Cys Ser Cys Lys Glu Asn Val Glu Gly Glu Asp Cys Ser Arg Cys Lys
           485                 490                 495

tct ggt ttc ttc aac ttg caa gaa gat aat cag aaa ggc tgt gag gag   1593
Ser Gly Phe Phe Asn Leu Gln Glu Asp Asn Gln Lys Gly Cys Glu Glu
       500                 505                 510

tgt ttc tgt tca gga gta tca aac aga tgt cag agt tcc tac tgg acc   1641
Cys Phe Cys Ser Gly Val Ser Asn Arg Cys Gln Ser Ser Tyr Trp Thr
   515                 520                 525

tat ggg aat att caa gac atg cgt ggt tgg tat ctc aca gac ctc tct   1689
Tyr Gly Asn Ile Gln Asp Met Arg Gly Trp Tyr Leu Thr Asp Leu Ser
530                 535                 540                 545

ggc cgc att cgg atg gct ccc cag ctt gat aac cct gac tca cct cag   1737
Gly Arg Ile Arg Met Ala Pro Gln Leu Asp Asn Pro Asp Ser Pro Gln
               550                 555                 560

cag atc agc atc agt aac tct gag gcc cgg aaa tcc ctg ctt gat ggt   1785
Gln Ile Ser Ile Ser Asn Ser Glu Ala Arg Lys Ser Leu Leu Asp Gly
           565                 570                 575

tac tac tgg agt gca ccg cct cca tat ctg gga aac aga ctt cca gct   1833
Tyr Tyr Trp Ser Ala Pro Pro Pro Tyr Leu Gly Asn Arg Leu Pro Ala
       580                 585                 590

gtt ggg gga cag ttg tca ttt acc atc tca tat gac ctc gaa gaa gag   1881
Val Gly Gly Gln Leu Ser Phe Thr Ile Ser Tyr Asp Leu Glu Glu Glu
   595                 600                 605

gaa gac gat aca gaa aaa ctc ctt cag ctg atg att atc ttt gag gga   1929
Glu Asp Asp Thr Glu Lys Leu Leu Gln Leu Met Ile Ile Phe Glu Gly
610                 615                 620                 625

aat gac tta aga atc agc aca gcg tat aag gag gtg tac tta gag cca   1977
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Asn Asp Leu Arg Ile Ser Thr Ala Tyr Lys Glu Val Tyr Leu Glu Pro
                630                 635                 640

tct gaa gaa cac gtt gag gag gtg tca ctc aaa gaa gag gcc ttt act   2025
Ser Glu Glu His Val Glu Glu Val Ser Leu Lys Glu Glu Ala Phe Thr
            645                 650                 655

ata cat gga aca aat ttg cca gtc act aga aaa gat ttc atg att gtt   2073
Ile His Gly Thr Asn Leu Pro Val Thr Arg Lys Asp Phe Met Ile Val
        660                 665                 670

ctc aca aat ttg gga gag atc ctt atc caa atc aca tac aac tta ggg   2121
Leu Thr Asn Leu Gly Glu Ile Leu Ile Gln Ile Thr Tyr Asn Leu Gly
    675                 680                 685

atg gac gcc atc ttc agg ctg agt tct gtc aat ctt gaa tct cct gtc   2169
Met Asp Ala Ile Phe Arg Leu Ser Ser Val Asn Leu Glu Ser Pro Val
690                 695                 700                 705

cct tat cct act gat aga cgt att gca act gat gtg gaa gtt tgc cag   2217
Pro Tyr Pro Thr Asp Arg Arg Ile Ala Thr Asp Val Glu Val Cys Gln
                710                 715                 720

tgt cca cct ggg tac agt ggc agc tct tgt gaa aca tgt tgg cct agg   2265
Cys Pro Pro Gly Tyr Ser Gly Ser Ser Cys Glu Thr Cys Trp Pro Arg
            725                 730                 735

cac cga aga gtt aac ggc acc att ttt ggt ggc att tgt gaa cca tgt   2313
His Arg Arg Val Asn Gly Thr Ile Phe Gly Gly Ile Cys Glu Pro Cys
        740                 745                 750

cag tgc ttt gct cat gca gaa gcc tgt gat gac atc aca gga gaa tgt   2361
Gln Cys Phe Ala His Ala Glu Ala Cys Asp Asp Ile Thr Gly Glu Cys
    755                 760                 765

ctg aac tgt aag gat cac aca ggt ggg ccg tac tgc aat gaa tgt ctc   2409
Leu Asn Cys Lys Asp His Thr Gly Gly Pro Tyr Cys Asn Glu Cys Leu
770                 775                 780                 785

cct gga ttc tat ggt gat cct act cga gga agc cct gaa gac tgt cag   2457
Pro Gly Phe Tyr Gly Asp Pro Thr Arg Gly Ser Pro Glu Asp Cys Gln
                790                 795                 800

ccc tgt gcc tgt cca ctc aat atc cca tca aat aac ttt agt cca aca   2505
Pro Cys Ala Cys Pro Leu Asn Ile Pro Ser Asn Asn Phe Ser Pro Thr
            805                 810                 815

tgc cat tta gac cgg agt ctg gga ttg atc tgt gac gag tgt cct att   2553
Cys His Leu Asp Arg Ser Leu Gly Leu Ile Cys Asp Glu Cys Pro Ile
        820                 825                 830

ggg tac aca gga ccg cgc tgt gag agg tgt gca gaa ggc tat ttt gga   2601
Gly Tyr Thr Gly Pro Arg Cys Glu Arg Cys Ala Glu Gly Tyr Phe Gly
    835                 840                 845

caa cct tcc gta cct gga gga tca tgt cag cca tgc caa tgc aat gac   2649
Gln Pro Ser Val Pro Gly Gly Ser Cys Gln Pro Cys Gln Cys Asn Asp
850                 855                 860                 865

aac ctt gac tac tcc atc cct ggc agc tgt gac agc ctg tct ggc tcc   2697
Asn Leu Asp Tyr Ser Ile Pro Gly Ser Cys Asp Ser Leu Ser Gly Ser
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                870                 875                 880

tgt ctg att tgt aag cca ggt aca aca ggc cgg tac tgt gag ctc tgt   2745
Cys Leu Ile Cys Lys Pro Gly Thr Thr Gly Arg Tyr Cys Glu Leu Cys
            885                 890                 895

gct gat ggg tat ttt gga gac gcg gtt aat aca aag aac tgt caa cca   2793
Ala Asp Gly Tyr Phe Gly Asp Ala Val Asn Thr Lys Asn Cys Gln Pro
        900                 905                 910

tgc cgt tgt gat atc aat ggc tcc ttc tca gag gat tgt cac aca aga   2841
Cys Arg Cys Asp Ile Asn Gly Ser Phe Ser Glu Asp Cys His Thr Arg
    915                 920                 925

act ggg caa tgt gag tgc aga ccc aat gtt cag ggg cgg cac tgt gac   2889
Thr Gly Gln Cys Glu Cys Arg Pro Asn Val Gln Gly Arg His Cys Asp
930                 935                 940                 945

gag tgt aag cct gaa acc ttt ggc ctg caa ctg gga agg ggt tgt ctg   2937
Glu Cys Lys Pro Glu Thr Phe Gly Leu Gln Leu Gly Arg Gly Cys Leu
                950                 955                 960

ccc tgc aac tgc aat tct ttt ggg tct aag tcc ttt gac tgt gaa gca   2985
Pro Cys Asn Cys Asn Ser Phe Gly Ser Lys Ser Phe Asp Cys Glu Ala
            965                 970                 975

agt ggg cag tgc tgg tgc cag cct gga gta gca ggg aag aaa tgt gac   3033
Ser Gly Gln Cys Trp Cys Gln Pro Gly Val Ala Gly Lys Lys Cys Asp
        980                 985                 990

cgt tgt gcc cat ggc tac ttc aac ttc caa gaa gga ggc tgc ata gct   3081
Arg Cys Ala His Gly Tyr Phe Asn Phe Gln Glu Gly Gly Cys Ile Ala
    995                1000                1005

tgt gac tgt tct cat ctg ggc aac aac tgt gac cca aaa act ggc caa   3129
Cys Asp Cys Ser His Leu Gly Asn Asn Cys Asp Pro Lys Thr Gly Gln
1010                1015                1020                1025

tgc att tgc cca ccc aat acc act gga gaa aag tgt tct gag tgt ctt   3177
Cys Ile Cys Pro Pro Asn Thr Thr Gly Glu Lys Cys Ser Glu Cys Leu
                1030                1035                1040

ccc aac acc tgg ggt cac agc att gtc acc ggc tgt aag gtt tgt aac   3225
Pro Asn Thr Trp Gly His Ser Ile Val Thr Gly Cys Lys Val Cys Asn
            1045                1050                1055

tgc agc act gtg ggg tcc ttg gct tct cag tgc aat gta aac acg ggc   3273
Cys Ser Thr Val Gly Ser Leu Ala Ser Gln Cys Asn Val Asn Thr Gly
        1060                1065                1070

cag tgc agc tgt cat cca aaa ttc tct ggt atg aaa tgc tca gag tgc   3321
Gln Cys Ser Cys His Pro Lys Phe Ser Gly Met Lys Cys Ser Glu Cys
    1075                1080                1085

agc cga ggt cac tgg aac tat cct ctc tgc act cta tgt gac tgc ttc   3369
Ser Arg Gly His Trp Asn Tyr Pro Leu Cys Thr Leu Cys Asp Cys Phe
1090                1095                1100                1105

ctt cca ggc aca gat gcc acg act tgt gat ctg gag act agg aaa tgc   3417
Leu Pro Gly Thr Asp Ala Thr Thr Cys Asp Leu Glu Thr Arg Lys Cys
                1110                1115                1120
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tcc tgt agt gat caa act gga cag tgc agc tgt aag gtg aat gtg gaa   3465
Ser Cys Ser Asp Gln Thr Gly Gln Cys Ser Cys Lys Val Asn Val Glu
          1125                1130                1135

ggc gtc cac tgt gac agg tgc cgg cct ggc aaa ttt gga cta gat gcc   3513
Gly Val His Cys Asp Arg Cys Arg Pro Gly Lys Phe Gly Leu Asp Ala
       1140                1145                1150

aag aac cca ctt ggc tgc agc agc tgc tac tgc ttt gga gtt act agt   3561
Lys Asn Pro Leu Gly Cys Ser Ser Cys Tyr Cys Phe Gly Val Thr Ser
   1155                1160                1165

caa tgc tct gaa gca aag ggg ctg atc cgt acg tgg gtg act ttg agt   3609
Gln Cys Ser Glu Ala Lys Gly Leu Ile Arg Thr Trp Val Thr Leu Ser
1170                1175                1180                1185

gat gaa cag acc att cta cct ctg gtg gat gag gcc ctg cag cac acg   3657
Asp Glu Gln Thr Ile Leu Pro Leu Val Asp Glu Ala Leu Gln His Thr
               1190                1195                1200

act acc aaa ggc att gct ttc cag aaa cca gag att gtt gca aag atg   3705
Thr Thr Lys Gly Ile Ala Phe Gln Lys Pro Glu Ile Val Ala Lys Met
          1205                1210                1215

gat gaa gtc agg caa gag ctc cat ttg gaa cct ttt tac tgg aaa ctc   3753
Asp Glu Val Arg Gln Glu Leu His Leu Glu Pro Phe Tyr Trp Lys Leu
       1220                1225                1230

cca caa caa ttt gaa ggg aaa aag ttg atg gct tat ggt ggc aaa ctc   3801
Pro Gln Gln Phe Glu Gly Lys Lys Leu Met Ala Tyr Gly Gly Lys Leu
   1235                1240                1245

aag tat gcc atc tat ttt gag gct cgg gat gag aca ggc ttt gcc aca   3849
Lys Tyr Ala Ile Tyr Phe Glu Ala Arg Asp Glu Thr Gly Phe Ala Thr
1250                1255                1260                1265

tat aaa cct caa gtt atc att cga ggt gga act cct act cat gct aga   3897
Tyr Lys Pro Gln Val Ile Ile Arg Gly Gly Thr Pro Thr His Ala Arg
               1270                1275                1280

att att acc aga cac atg gct gcc cct ctc att ggc cag ttg aca cgg   3945
Ile Ile Thr Arg His Met Ala Ala Pro Leu Ile Gly Gln Leu Thr Arg
          1285                1290                1295

cat gaa ata gaa atg aca gag aaa gaa tgg aaa tat tat ggt gat gat   3993
His Glu Ile Glu Met Thr Glu Lys Glu Trp Lys Tyr Tyr Gly Asp Asp
       1300                1305                1310

cct cga atc agt aga act gtg acc cgt gaa gac ttc ttg gat ata cta   4041
Pro Arg Ile Ser Arg Thr Val Thr Arg Glu Asp Phe Leu Asp Ile Leu
   1315                1320                1325

tat gat att cac tat atc ctt atc aag gct act tat gga aac gtt gtg   4089
Tyr Asp Ile His Tyr Ile Leu Ile Lys Ala Thr Tyr Gly Asn Val Val
1330                1335                1340                1345

aga caa agc cgc att tct gaa atc tcc atg gaa gta gct gaa cca gga   4137
Arg Gln Ser Arg Ile Ser Glu Ile Ser Met Glu Val Ala Glu Pro Gly
               1350                1355                1360
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cat gta tta gca ggg agc cca cca gca cac ttg ata gaa aga tgc gat   4185
His Val Leu Ala Gly Ser Pro Pro Ala His Leu Ile Glu Arg Cys Asp
          1365                1370                1375

tgc cct cct ggc tat tct ggc ttg tct tgt gag acg tgt gca cca gga   4233
Cys Pro Pro Gly Tyr Ser Gly Leu Ser Cys Glu Thr Cys Ala Pro Gly
       1380                1385                1390

ttt tac cga ctt cgt tct gaa cca ggt ggg cgg act cct gga cca acc   4281
Phe Tyr Arg Leu Arg Ser Glu Pro Gly Gly Arg Thr Pro Gly Pro Thr
   1395                1400                1405

tta ggg acc tgt gtt ccc tgc caa tgt aat gga cac agc agt cag tgt   4329
Leu Gly Thr Cys Val Pro Cys Gln Cys Asn Gly His Ser Ser Gln Cys
1410                1415                1420                1425

gat cct gag acc tca gta tgc cag aat tgt cag cat cac act gct ggt   4377
Asp Pro Glu Thr Ser Val Cys Gln Asn Cys Gln His His Thr Ala Gly
               1430                1435                1440

gac ttc tgt gag cgc tgt gcc ctt ggc tac tat gga atc gtc agg gga   4425
Asp Phe Cys Glu Arg Cys Ala Leu Gly Tyr Tyr Gly Ile Val Arg Gly
          1445                1450                1455

ttg cca aat gac tgc caa cca tgt gct tgt cct ctg att tcg ccc agc   4473
Leu Pro Asn Asp Cys Gln Pro Cys Ala Cys Pro Leu Ile Ser Pro Ser
       1460                1465                1470

aac aat ttc agc ccc tct tgt gta ttg gaa ggt ctg gaa gat tac cgt   4521
Asn Asn Phe Ser Pro Ser Cys Val Leu Glu Gly Leu Glu Asp Tyr Arg
   1475                1480                1485

tgc acc gcc tgc cca agg ggc tat gaa gga cag tac tgt gaa agg tgt   4569
Cys Thr Ala Cys Pro Arg Gly Tyr Glu Gly Gln Tyr Cys Glu Arg Cys
1490                1495                1500                1505

gcc cca ggc tat act ggc agc cca agc agc ccc gga ggc tcc tgc caa   4617
Ala Pro Gly Tyr Thr Gly Ser Pro Ser Ser Pro Gly Gly Ser Cys Gln
               1510                1515                1520

gaa tgt gag tgt gac cct tat ggc tcc cta ccg gtt ccc tgt gac cgg   4665
Glu Cys Glu Cys Asp Pro Tyr Gly Ser Leu Pro Val Pro Cys Asp Arg
          1525                1530                1535

gtc aca gga ctc tgc acg tgc cgc cct gga gcc aca gga agg aag tgt   4713
Val Thr Gly Leu Cys Thr Cys Arg Pro Gly Ala Thr Gly Arg Lys Cys
       1540                1545                1550

gat ggc tgc gag cac tgg cat gca cgc gag ggt gca gag tgt gtc ttt   4761
Asp Gly Cys Glu His Trp His Ala Arg Glu Gly Ala Glu Cys Val Phe
   1555                1560                1565

tgt gga gac gag tgt aca ggc ctt ctt ctt ggt gac ctg gct cgt cta   4809
Cys Gly Asp Glu Cys Thr Gly Leu Leu Leu Gly Asp Leu Ala Arg Leu
1570                1575                1580                1585

gag cag atg acc atg aac atc aac ctc acg ggc cca ctg cct gct cca   4857
Glu Gln Met Thr Met Asn Ile Asn Leu Thr Gly Pro Leu Pro Ala Pro
               1590                1595                1600

tat aaa att ctg tat ggt ctt gaa aat aca act cag gaa ctc aag cac   4905
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Tyr Lys Ile Leu Tyr Gly Leu Glu Asn Thr Thr Gln Glu Leu Lys His
          1605                1610                1615

ctg cta tca ccg caa cgg gca cca gag agg ctc att cag ttg gca gag   4953
Leu Leu Ser Pro Gln Arg Ala Pro Glu Arg Leu Ile Gln Leu Ala Glu
       1620                1625                1630

ggc aac gtg aac aca ctt gtg atg gaa aca aat gag ctg cta acc aga   5001
Gly Asn Val Asn Thr Leu Val Met Glu Thr Asn Glu Leu Leu Thr Arg
   1635                1640                1645

gca acc aaa gtg aca gca gat ggt gag caa aca gga caa gat gct gag   5049
Ala Thr Lys Val Thr Ala Asp Gly Glu Gln Thr Gly Gln Asp Ala Glu
1650                1655                1660                1665

agg acc aac tcc aga gca gaa tcc ttg gaa gaa ttc att aaa ggg ctt   5097
Arg Thr Asn Ser Arg Ala Glu Ser Leu Glu Glu Phe Ile Lys Gly Leu
               1670                1675                1680

gtc cag gat gct gaa gcc ata aat gaa aaa gct gta aaa cta aat gaa   5145
Val Gln Asp Ala Glu Ala Ile Asn Glu Lys Ala Val Lys Leu Asn Glu
          1685                1690                1695

acc tta gga aat caa gat aag aca gca gag aga aac ttg gag gag ctt   5193
Thr Leu Gly Asn Gln Asp Lys Thr Ala Glu Arg Asn Leu Glu Glu Leu
       1700                1705                1710

caa aag gaa atc gac cgg atg ctg aag gaa ctg aga agt aaa gat ctt   5241
Gln Lys Glu Ile Asp Arg Met Leu Lys Glu Leu Arg Ser Lys Asp Leu
   1715                1720                1725

caa aca cag aag gaa gtt gct gag gat gag ctc gtg gca gca gaa ggc   5289
Gln Thr Gln Lys Glu Val Ala Glu Asp Glu Leu Val Ala Ala Glu Gly
1730                1735                1740                1745

ctt ctg aag aga gta aac aag ctg ttt gga gag ccc aga gcc cag aat   5337
Leu Leu Lys Arg Val Asn Lys Leu Phe Gly Glu Pro Arg Ala Gln Asn
               1750                1755                1760

gaa gat atg gaa aag gat ctc cag cag aaa ctg gca gag tac aag aac   5385
Glu Asp Met Glu Lys Asp Leu Gln Gln Lys Leu Ala Glu Tyr Lys Asn
          1765                1770                1775

aaa ctt gat gat gct tgg gat cta ttg aga gaa gcc act gat aaa acc   5433
Lys Leu Asp Asp Ala Trp Asp Leu Leu Arg Glu Ala Thr Asp Lys Thr
       1780                1785                1790

cga gat gct aat cgt ttg tct gct gcc aat caa aaa aac atg acc ata   5481
Arg Asp Ala Asn Arg Leu Ser Ala Ala Asn Gln Lys Asn Met Thr Ile
   1795                1800                1805

ctg gag aca aag aag gag gct att gaa ggt agc aaa cga caa ata gag   5529
Leu Glu Thr Lys Lys Glu Ala Ile Glu Gly Ser Lys Arg Gln Ile Glu
1810                1815                1820                1825

aac act tta aag gaa ggc aat gac atc ctt gat gaa gcc aat caa ctc   5577
Asn Thr Leu Lys Glu Gly Asn Asp Ile Leu Asp Glu Ala Asn Gln Leu
               1830                1835                1840

tta ggt gaa atc aac tca gtc ata gat tat gtc gac gac att aaa act   5625
Leu Gly Glu Ile Asn Ser Val Ile Asp Tyr Val Asp Asp Ile Lys Thr
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          1845                1850                1855

aag ttg cca cca atg tcc gag gag ctg agt gac aaa ata gat gac ctc   5673
Lys Leu Pro Pro Met Ser Glu Glu Leu Ser Asp Lys Ile Asp Asp Leu
       1860                1865                1870

gcc cag gaa ata aag gac aga agg ctt gct gag aag gtg ttc cag gct   5721
Ala Gln Glu Ile Lys Asp Arg Arg Leu Ala Glu Lys Val Phe Gln Ala
   1875                1880                1885

gag agc cat gct gct cag ctg aac gac tcg tct gct gta ctt gat gga   5769
Glu Ser His Ala Ala Gln Leu Asn Asp Ser Ser Ala Val Leu Asp Gly
1890                1895                1900                1905

atc ctg gat gag gct aag aac atc tct ttc aat gcc acg gca gcc ttc   5817
Ile Leu Asp Glu Ala Lys Asn Ile Ser Phe Asn Ala Thr Ala Ala Phe
              1910                1915                1920

aga gct tac agt aat att aaa gac tac att gat gaa gct gag aaa gtg   5865
Arg Ala Tyr Ser Asn Ile Lys Asp Tyr Ile Asp Glu Ala Glu Lys Val
          1925                1930                1935

gcc aga gaa gcc aaa gag ctt gcc caa ggg gct aca aaa ctg gca aca   5913
Ala Arg Glu Ala Lys Glu Leu Ala Gln Gly Ala Thr Lys Leu Ala Thr
       1940                1945                1950

agt cct cag ggc tta tta aaa gaa gat gcc aaa ggc tcc ctt cag aaa   5961
Ser Pro Gln Gly Leu Leu Lys Glu Asp Ala Lys Gly Ser Leu Gln Lys
   1955                1960                1965

agc ttc agg atc ctc aat gaa gcc aag aag cta gca aac gat gtg aaa   6009
Ser Phe Arg Ile Leu Asn Glu Ala Lys Lys Leu Ala Asn Asp Val Lys
1970                1975                1980                1985

gga aat cac aat gat cta aat gac ctg aaa acc agg tta gaa act gct   6057
Gly Asn His Asn Asp Leu Asn Asp Leu Lys Thr Arg Leu Glu Thr Ala
              1990                1995                2000

gac ctt aga aac agt gga ctt cta gga gct cta aat gac acc atg gac   6105
Asp Leu Arg Asn Ser Gly Leu Leu Gly Ala Leu Asn Asp Thr Met Asp
          2005                2010                2015

aag tta tca gcc att aca aat gac acg gct gct aaa ctg cag gct gtc   6153
Lys Leu Ser Ala Ile Thr Asn Asp Thr Ala Ala Lys Leu Gln Ala Val
       2020                2025                2030

aaa gag aaa gcc aga gaa gcc aat gac aca gca aaa gct gtc ctg gcc   6201
Lys Glu Lys Ala Arg Glu Ala Asn Asp Thr Ala Lys Ala Val Leu Ala
   2035                2040                2045

cag gtt aag gac ctg cat cag aac cta gat ggc ctg aag caa aac tac   6249
Gln Val Lys Asp Leu His Gln Asn Leu Asp Gly Leu Lys Gln Asn Tyr
2050                2055                2060                2065

aat aaa ctg gca gac agc gtg gcc aaa acg aac gct gtg gtg aaa gat   6297
Asn Lys Leu Ala Asp Ser Val Ala Lys Thr Asn Ala Val Val Lys Asp
              2070                2075                2080

cct tcc aaa aac aaa atc att gca gat gca ggc act tcc gtg aga aat   6345
Pro Ser Lys Asn Lys Ile Ile Ala Asp Ala Gly Thr Ser Val Arg Asn
          2085                2090                2095
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cta gaa cag gaa gct gac cgg cta atc gac aaa ctc aag ccc atc aag   6393
Leu Glu Gln Glu Ala Asp Arg Leu Ile Asp Lys Leu Lys Pro Ile Lys
       2100                2105                2110

gag ctt gag gac aac cta aag aaa aac att tct gaa ata aag gaa ctg   6441
Glu Leu Glu Asp Asn Leu Lys Lys Asn Ile Ser Glu Ile Lys Glu Leu
   2115                2120                2125

atc aac caa gct cgg aaa caa gct aac tct atc aaa gta tct gtt tct   6489
Ile Asn Gln Ala Arg Lys Gln Ala Asn Ser Ile Lys Val Ser Val Ser
2130                2135                2140                2145

tcg gga ggt gac tgt gtt cgg aca tac agg cca gaa atc aag aaa gga   6537
Ser Gly Gly Asp Cys Val Arg Thr Tyr Arg Pro Glu Ile Lys Lys Gly
               2150                2155                2160

agc tac aat aac atc gtt gtc cat gtc aag acc gct gtt gcc gac aac   6585
Ser Tyr Asn Asn Ile Val Val His Val Lys Thr Ala Val Ala Asp Asn
           2165                2170                2175

ctc ctt ttt tat ctt gga agt gcc aaa ttt att gac ttt ctt gct ata   6633
Leu Leu Phe Tyr Leu Gly Ser Ala Lys Phe Ile Asp Phe Leu Ala Ile
       2180                2185                2190

gaa atg cgc aaa ggc aaa gtc agc ttc ctc tgg att gtt ggc tct gga   6681
Glu Met Arg Lys Gly Lys Val Ser Phe Leu Trp Ile Val Gly Ser Gly
   2195                2200                2205

gtt ggc cga gta ggg ttt cca gac ttg acc atc gac gac tcc tat tgg   6729
Val Gly Arg Val Gly Phe Pro Asp Leu Thr Ile Asp Asp Ser Tyr Trp
2210                2215                2220                2225

tac cgt att gaa gca tca aga acg gga aga aat gga tct att tct gtg   6777
Tyr Arg Ile Glu Ala Ser Arg Thr Gly Arg Asn Gly Ser Ile Ser Val
               2230                2235                2240

aga gct tta gat gga ccc aaa gcc agt atg gta ccc agc acc tac cat   6825
Arg Ala Leu Asp Gly Pro Lys Ala Ser Met Val Pro Ser Thr Tyr His
           2245                2250                2255

tca gtg tct cct ccc ggg tat act atc cta gat gtg gat gca aat gca   6873
Ser Val Ser Pro Pro Gly Tyr Thr Ile Leu Asp Val Asp Ala Asn Ala
       2260                2265                2270

atg ctg ttt gtt ggt ggc ctg acc gga aaa ata aag aag gcc gat gct   6921
Met Leu Phe Val Gly Gly Leu Thr Gly Lys Ile Lys Lys Ala Asp Ala
   2275                2280                2285

gta cgt gtg atc acc ttc acc ggc tgt atg gga gaa aca tac ttt gac   6969
Val Arg Val Ile Thr Phe Thr Gly Cys Met Gly Glu Thr Tyr Phe Asp
2290                2295                2300                2305

aac aaa cct ata ggt tta tgg aac ttc cgg gag aaa gaa ggc gac tgt   7017
Asn Lys Pro Ile Gly Leu Trp Asn Phe Arg Glu Lys Glu Gly Asp Cys
               2310                2315                2320

aag gga tgt act gtc agc cca caa gtg gaa gat agt gag ggg act att   7065
Lys Gly Cys Thr Val Ser Pro Gln Val Glu Asp Ser Glu Gly Thr Ile
           2325                2330                2335
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cag ttt gat ggt gaa ggc tat gca tta gtg agc cgg ccc atc cgc tgg   7113
Gln Phe Asp Gly Glu Gly Tyr Ala Leu Val Ser Arg Pro Ile Arg Trp
       2340                2345                2350

tac ccc aac atc tcc aca gtc atg ttc aag ttc cgg aca ttt tca tca   7161
Tyr Pro Asn Ile Ser Thr Val Met Phe Lys Phe Arg Thr Phe Ser Ser
   2355                2360                2365

agt gct ctc ctg atg tat ctt gcc aca cga gac ctg aaa gat ttc atg   7209
Ser Ala Leu Leu Met Tyr Leu Ala Thr Arg Asp Leu Lys Asp Phe Met
2370                2375                2380                2385

agt gta gag ctc agt gat gga cat gtg aaa gtc agc tat gac ctg ggc   7257
Ser Val Glu Leu Ser Asp Gly His Val Lys Val Ser Tyr Asp Leu Gly
               2390                2395                2400

tca gga atg act tcc gtt gtc agc aat caa aac cat aat gat ggg aaa   7305
Ser Gly Met Thr Ser Val Val Ser Asn Gln Asn His Asn Asp Gly Lys
          2405                2410                2415

tgg aaa gca ttc acg ctg tcg cgg att cag aaa caa gcc aac ata tcg   7353
Trp Lys Ala Phe Thr Leu Ser Arg Ile Gln Lys Gln Ala Asn Ile Ser
       2420                2425                2430

att gtc gac atc gat tct aac cag gag gag aat gta gct act tca tct   7401
Ile Val Asp Ile Asp Ser Asn Gln Glu Glu Asn Val Ala Thr Ser Ser
   2435                2440                2445

tct gga aac aac ttt ggt ctt gac ttg aaa gca gat gac aaa ata tat   7449
Ser Gly Asn Asn Phe Gly Leu Asp Leu Lys Ala Asp Asp Lys Ile Tyr
2450                2455                2460                2465

ttt ggt ggc ctg cca act ctg aga aac ttg agt atg aaa gca agg cca   7497
Phe Gly Gly Leu Pro Thr Leu Arg Asn Leu Ser Met Lys Ala Arg Pro
               2470                2475                2480

gaa gtc aat gtg aag aaa tac tcc ggc tgc ctc aaa gat att gaa att   7545
Glu Val Asn Val Lys Lys Tyr Ser Gly Cys Leu Lys Asp Ile Glu Ile
          2485                2490                2495

tca aga aca cct tac aat ata ctc agc agc cct gat tat gtt ggt gtg   7593
Ser Arg Thr Pro Tyr Asn Ile Leu Ser Ser Pro Asp Tyr Val Gly Val
       2500                2505                2510

acc aaa ggc tgt tca ctg gag aat gtt aat aca gtt agt ttc ccc aag   7641
Thr Lys Gly Cys Ser Leu Glu Asn Val Asn Thr Val Ser Phe Pro Lys
   2515                2520                2525

cct ggt ttt gtg gag ctt gcc gct gtg tct att gat gtt gga aca gaa   7689
Pro Gly Phe Val Glu Leu Ala Ala Val Ser Ile Asp Val Gly Thr Glu
2530                2535                2540                2545

atc aat ctg tcc ttt agt acc agg aac gag tct ggg atc att ctc ttg   7737
Ile Asn Leu Ser Phe Ser Thr Arg Asn Glu Ser Gly Ile Ile Leu Leu
               2550                2555                2560

gga agt gga ggg aca ctc aca cca ccc agg aga aaa cgg aga caa acc   7785
Gly Ser Gly Gly Thr Leu Thr Pro Pro Arg Arg Lys Arg Arg Gln Thr
          2565                2570                2575

aca cag gct tat tat gcc ata ttc ctc aac aag ggc cgc ttg gaa gtg   7833
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Thr Gln Ala Tyr Tyr Ala Ile Phe Leu Asn Lys Gly Arg Leu Glu Val
       2580                2585                2590

cat ctc tcc tcg ggg aca cgg aca atg agg aaa att gtc atc aaa ccg   7881
His Leu Ser Ser Gly Thr Arg Thr Met Arg Lys Ile Val Ile Lys Pro
   2595                2600                2605

gag cca aat ttg ttt cat gat ggg aga gaa cat tct gtc cac gta gaa   7929
Glu Pro Asn Leu Phe His Asp Gly Arg Glu His Ser Val His Val Glu
2610                2615                2620                2625

aga acc aga ggc atc ttc act gtt caa att gat gaa gac aga aga cat   7977
Arg Thr Arg Gly Ile Phe Thr Val Gln Ile Asp Glu Asp Arg Arg His
               2630                2635                2640

atc caa aac ctg aca gag gaa cag ccc atc gaa gtg aaa aag ctc ttt   8025
Ile Gln Asn Leu Thr Glu Glu Gln Pro Ile Glu Val Lys Lys Leu Phe
           2645                2650                2655

gtc ggg ggt gct cct cct gaa ttt cag ccc tcc cca ctc agg aat att   8073
Val Gly Gly Ala Pro Pro Glu Phe Gln Pro Ser Pro Leu Arg Asn Ile
       2660                2665                2670

ccg gcc ttt caa ggc tgt gtg tgg aac ctt gtt att aac tcc atc ccc   8121
Pro Ala Phe Gln Gly Cys Val Trp Asn Leu Val Ile Asn Ser Ile Pro
   2675                2680                2685

atg gac ttt gcg cag cct ata gcc ttc aaa aat gcc gac att ggt cgc   8169
Met Asp Phe Ala Gln Pro Ile Ala Phe Lys Asn Ala Asp Ile Gly Arg
2690                2695                2700                2705

tgt acc tat caa aag ccc cgg gaa gat gag agt gaa gca gtt cca gct   8217
Cys Thr Tyr Gln Lys Pro Arg Glu Asp Glu Ser Glu Ala Val Pro Ala
               2710                2715                2720

gaa gtt att gtc cag cct cag tcg gtg ccc acc cct gcc ttc cct ttc   8265
Glu Val Ile Val Gln Pro Gln Ser Val Pro Thr Pro Ala Phe Pro Phe
           2725                2730                2735

cca gtc ccc acc atg gtg cat ggc cct tgt gtt gca gaa tca gaa cca   8313
Pro Val Pro Thr Met Val His Gly Pro Cys Val Ala Glu Ser Glu Pro
       2740                2745                2750

gct ctt ctg aca ggg agc aag cag ttt ggg ctt tcc aga aac agc cac   8361
Ala Leu Leu Thr Gly Ser Lys Gln Phe Gly Leu Ser Arg Asn Ser His
   2755                2760                2765

att gca att gtc ttt gat gac acc aaa gtt aaa aac cgc ctc acc att   8409
Ile Ala Ile Val Phe Asp Asp Thr Lys Val Lys Asn Arg Leu Thr Ile
2770                2775                2780                2785

gag ctg gag gta cga act gaa gct gaa tca ggc ttg ctc ttc tac atg   8457
Glu Leu Glu Val Arg Thr Glu Ala Glu Ser Gly Leu Leu Phe Tyr Met
               2790                2795                2800

ggt cgg atc aat cat gct gat ttt ggt act gtt cag ctg agg aat ggg   8505
Gly Arg Ile Asn His Ala Asp Phe Gly Thr Val Gln Leu Arg Asn Gly
           2805                2810                2815

ttc ccg ttc ttc agt tat gat ttg ggg agt ggg agc acc aga acc atg   8553
Phe Pro Phe Phe Ser Tyr Asp Leu Gly Ser Gly Ser Thr Arg Thr Met
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      2820                2825                2830

atc ccc aca aaa atc aac gat ggt cag tgg cac aag att aag att gtg   8601
Ile Pro Thr Lys Ile Asn Asp Gly Gln Trp His Lys Ile Lys Ile Val
   2835                2840                2845

aga gtg aag cag gag gga att ctt tat gtg gat gat gcc tcc agc caa   8649
Arg Val Lys Gln Glu Gly Ile Leu Tyr Val Asp Asp Ala Ser Ser Gln
2850                2855                2860                2865

acc atc agt ccc aag aaa gcc gac atc ctg gat gtc ggg ggg att ctg   8697
Thr Ile Ser Pro Lys Lys Ala Asp Ile Leu Asp Val Gly Gly Ile Leu
               2870                2875                2880

tat gtc ggt gga ttg ccg atc aac tat acc aca cgc aga att ggt cca   8745
Tyr Val Gly Gly Leu Pro Ile Asn Tyr Thr Thr Arg Arg Ile Gly Pro
          2885                2890                2895

gtg act tac agc ctg gat ggc tgt gtt agg aat ctt cac atg gaa caa   8793
Val Thr Tyr Ser Leu Asp Gly Cys Val Arg Asn Leu His Met Glu Gln
       2900                2905                2910

gcc cct gtt gat ctg gac cag cct acc tcc agc ttt cac gtt ggg aca   8841
Ala Pro Val Asp Leu Asp Gln Pro Thr Ser Ser Phe His Val Gly Thr
   2915                2920                2925

tgc ttt gcg aat gca gag agt ggg act tac ttt gat gga acc ggt ttt   8889
Cys Phe Ala Asn Ala Glu Ser Gly Thr Tyr Phe Asp Gly Thr Gly Phe
2930                2935                2940                2945

ggt aaa gca gtt ggt ggg ttc atc gtt gga ttg gac ctt ctt gtg gaa   8937
Gly Lys Ala Val Gly Gly Phe Ile Val Gly Leu Asp Leu Leu Val Glu
               2950                2955                2960

ttt gaa ttc cgt acc aca aga ccc act ggg gtc ctc ctg ggg atc agc   8985
Phe Glu Phe Arg Thr Thr Arg Pro Thr Gly Val Leu Leu Gly Ile Ser
          2965                2970                2975

agt cag aag atg gat gga atg ggt att gaa atg atc gac gag aag ctt   9033
Ser Gln Lys Met Asp Gly Met Gly Ile Glu Met Ile Asp Glu Lys Leu
       2980                2985                2990

atg ttc cac gtg gat aat ggc gct ggc cga ttc act gca att tat gat   9081
Met Phe His Val Asp Asn Gly Ala Gly Arg Phe Thr Ala Ile Tyr Asp
   2995                3000                3005

gct gag atc cca ggc cac atg tgc aat gga cag tgg tat aaa gtc act   9129
Ala Glu Ile Pro Gly His Met Cys Asn Gly Gln Trp Tyr Lys Val Thr
3010                3015                3020                3025

gcc aag aag atc aaa aac cgt ctt gag ctg gtg gta gat ggg aac cag   9177
Ala Lys Lys Ile Lys Asn Arg Leu Glu Leu Val Val Asp Gly Asn Gln
               3030                3035                3040

gtg gat gcc cag agc cca aac tca gca tcg aca tca gct gat aca aac   9225
Val Asp Ala Gln Ser Pro Asn Ser Ala Ser Thr Ser Ala Asp Thr Asn
          3045                3050                3055

gac cct gtt ttc gtt ggc ggt ttc cca ggt ggc ctc aat cag ttt ggc   9273
Asp Pro Val Phe Val Gly Gly Phe Pro Gly Gly Leu Asn Gln Phe Gly
       3060                3065                3070
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```
ctg acc acc aac att agg ttc cga ggc tgc atc cga tct ctg aag ctc   9321
Leu Thr Thr Asn Ile Arg Phe Arg Gly Cys Ile Arg Ser Leu Lys Leu
   3075                3080                3085

acc aaa ggc act gca aac cgc tgg agg tta att ttg cca agg ccc tgg   9369
Thr Lys Gly Thr Ala Asn Arg Trp Arg Leu Ile Leu Pro Arg Pro Trp
3090              3095                3100                3105

aac tgaggggtgt tcaacctgta tcatgcccga ctacctaata aagatagttc        9422
Asn

aatcctgagg agaattcatc aaaacaagta tatcaagtta aacaatatac actcctatca 9482

tattaataaa actaatgtgc agcggccgc                                   9511


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  1               5                  10                  15

Leu Glu Gly Ser Gln Thr Gln Arg Arg Gln Ser Gln Ala His Gln Gln
            20                  25                  30

Arg Gly Leu Phe Pro Ala Val Leu Asn Leu Ala Ser Asn Ala Leu Ile
         35                  40                  45

Thr Thr Asn Ala Thr Cys Gly Glu Lys Gly Pro Glu Met Tyr Cys Lys
     50                  55                  60

Leu Val Glu His Val Pro Gly Gln Pro Val Arg Asn Pro Gln Cys Arg
 65                  70                  75                  80

Ile Cys Asn Gln Asn Ser Ser Asn Pro Tyr Gln Arg His Pro Ile Thr
                85                  90                  95

Asn Ala Ile Asp Gly Lys Asn Thr Trp Trp Gln Ser Pro Ser Ile Lys
            100                 105                 110

Asn Gly Val Glu Tyr His Tyr Val Thr Ile Thr Leu Asp Leu Gln Gln
        115                 120                 125

Val Phe Gln Ile Ala Tyr Val Ile Val Lys Ala Ala Asn Ser Pro Arg
    130                 135                 140

Pro Gly Asn Trp Ile Leu Glu Arg Ser Leu Asp Asp Val Glu Tyr Lys
145                 150                 155                 160

Pro Trp Gln Tyr His Ala Val Thr Asp Thr Glu Cys Leu Thr Leu Tyr
                165                 170                 175

Asn Ile Tyr Pro Arg Thr Gly Pro Pro Ser Tyr Ala Lys Asp Asp Glu
            180                 185                 190

Val Ile Cys Thr Ser Phe Tyr Ser Lys Ile His Pro Leu Glu Asn Gly
        195                 200                 205
```

```
Glu Ile His Ile Ser Leu Ile Asn Gly Arg Pro Ser Ala Asp Asp Pro
    210                 215                 220

Ser Pro Glu Leu Leu Glu Phe Thr Ser Ala Arg Tyr Ile Arg Leu Arg
225                 230                 235                 240

Phe Gln Arg Ile Arg Thr Leu Asn Ala Asp Leu Met Met Phe Ala His
                245                 250                 255

Lys Asp Pro Arg Glu Ile Asp Pro Ile Val Thr Arg Arg Tyr Tyr Tyr
            260                 265                 270

Ser Val Lys Asp Ile Ser Val Gly Gly Met Cys Ile Cys Tyr Gly His
        275                 280                 285

Ala Arg Ala Cys Pro Leu Asp Pro Ala Thr Asn Lys Ser Arg Cys Glu
    290                 295                 300

Cys Glu His Asn Thr Cys Gly Glu Ser Cys Asp Arg Cys Cys Pro Gly
305                 310                 315                 320

Phe His Gln Lys Pro Trp Arg Ala Gly Thr Phe Leu Thr Lys Ser Glu
                325                 330                 335

Cys Glu Ala Cys Asn Cys His Gly Lys Ala Glu Glu Cys Tyr Tyr Asp
            340                 345                 350

Glu Thr Val Ala Ser Arg Asn Leu Ser Leu Asn Ile His Gly Lys Tyr
        355                 360                 365

Ile Gly Gly Gly Val Cys Ile Asn Cys Thr His Asn Thr Ala Gly Ile
    370                 375                 380

Asn Cys Glu Thr Cys Val Asp Gly Phe Phe Arg Pro Lys Gly Val Ser
385                 390                 395                 400

Pro Asn Tyr Pro Arg Pro Cys Gln Pro Cys His Cys Asp Pro Thr Gly
                405                 410                 415

Ser Leu Ser Glu Val Cys Val Lys Asp Glu Lys Tyr Ala Gln Arg Gly
            420                 425                 430

Leu Lys Pro Gly Ser Cys His Cys Lys Thr Gly Phe Gly Gly Val Asn
        435                 440                 445

Cys Asp Arg Cys Val Arg Gly Tyr His Gly Tyr Pro Asp Cys Gln Pro
    450                 455                 460

Cys Asn Cys Ser Gly Leu Gly Ser Thr Asn Glu Asp Pro Cys Val Gly
465                 470                 475                 480

Pro Cys Ser Cys Lys Glu Asn Val Glu Gly Glu Asp Cys Ser Arg Cys
                485                 490                 495

Lys Ser Gly Phe Phe Asn Leu Gln Glu Asp Asn Gln Lys Gly Cys Glu
            500                 505                 510

Glu Cys Phe Cys Ser Gly Val Ser Asn Arg Cys Gln Ser Ser Tyr Trp
        515                 520                 525
```

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Thr Tyr Gly Asn Ile Gln Asp Met Arg Gly Trp Tyr Leu Thr Asp Leu
    530                 535                 540

Ser Gly Arg Ile Arg Met Ala Pro Gln Leu Asp Asn Pro Asp Ser Pro
545                 550                 555                 560

Gln Gln Ile Ser Ile Ser Asn Ser Glu Ala Arg Lys Ser Leu Leu Asp
                565                 570                 575

Gly Tyr Tyr Trp Ser Ala Pro Pro Pro Tyr Leu Gly Asn Arg Leu Pro
            580                 585                 590

Ala Val Gly Gly Gln Leu Ser Phe Thr Ile Ser Tyr Asp Leu Glu Glu
        595                 600                 605

Glu Glu Asp Asp Thr Glu Lys Leu Leu Gln Leu Met Ile Ile Phe Glu
    610                 615                 620

Gly Asn Asp Leu Arg Ile Ser Thr Ala Tyr Lys Glu Val Tyr Leu Glu
625                 630                 635                 640

Pro Ser Glu Glu His Val Glu Glu Val Ser Leu Lys Glu Glu Ala Phe
                645                 650                 655

Thr Ile His Gly Thr Asn Leu Pro Val Thr Arg Lys Asp Phe Met Ile
            660                 665                 670

Val Leu Thr Asn Leu Gly Glu Ile Leu Ile Gln Ile Thr Tyr Asn Leu
        675                 680                 685

Gly Met Asp Ala Ile Phe Arg Leu Ser Ser Val Asn Leu Glu Ser Pro
    690                 695                 700

Val Pro Tyr Pro Thr Asp Arg Arg Ile Ala Thr Asp Val Glu Val Cys
705                 710                 715                 720

Gln Cys Pro Pro Gly Tyr Ser Gly Ser Ser Cys Glu Thr Cys Trp Pro
                725                 730                 735

Arg His Arg Arg Val Asn Gly Thr Ile Phe Gly Gly Ile Cys Glu Pro
            740                 745                 750

Cys Gln Cys Phe Ala His Ala Glu Ala Cys Asp Asp Ile Thr Gly Glu
        755                 760                 765

Cys Leu Asn Cys Lys Asp His Thr Gly Gly Pro Tyr Cys Asn Glu Cys
    770                 775                 780

Leu Pro Gly Phe Tyr Gly Asp Pro Thr Arg Gly Ser Pro Glu Asp Cys
785                 790                 795                 800

Gln Pro Cys Ala Cys Pro Leu Asn Ile Pro Ser Asn Asn Phe Ser Pro
                805                 810                 815

Thr Cys His Leu Asp Arg Ser Leu Gly Leu Ile Cys Asp Glu Cys Pro
            820                 825                 830

Ile Gly Tyr Thr Gly Pro Arg Cys Glu Arg Cys Ala Glu Gly Tyr Phe
        835                 840                 845

Gly Gln Pro Ser Val Pro Gly Gly Ser Cys Gln Pro Cys Gln Cys Asn
```

```
    850                 855                 860

Asp Asn Leu Asp Tyr Ser Ile Pro Gly Ser Cys Asp Ser Leu Ser Gly
865                 870                 875                 880

Ser Cys Leu Ile Cys Lys Pro Gly Thr Thr Gly Arg Tyr Cys Glu Leu
                885                 890                 895

Cys Ala Asp Gly Tyr Phe Gly Asp Ala Val Asn Thr Lys Asn Cys Gln
            900                 905                 910

Pro Cys Arg Cys Asp Ile Asn Gly Ser Phe Ser Glu Asp Cys His Thr
        915                 920                 925

Arg Thr Gly Gln Cys Glu Cys Arg Pro Asn Val Gln Gly Arg His Cys
    930                 935                 940

Asp Glu Cys Lys Pro Glu Thr Phe Gly Leu Gln Leu Gly Arg Gly Cys
945                 950                 955                 960

Leu Pro Cys Asn Cys Asn Ser Phe Gly Ser Lys Ser Phe Asp Cys Glu
                965                 970                 975

Ala Ser Gly Gln Cys Trp Cys Gln Pro Gly Val Ala Gly Lys Lys Cys
            980                 985                 990

Asp Arg Cys Ala His Gly Tyr Phe Asn Phe Gln Glu Gly Gly Cys Ile
        995                1000                1005

Ala Cys Asp Cys Ser His Leu Gly Asn Asn Cys Asp Pro Lys Thr Gly
    1010                1015                1020

Gln Cys Ile Cys Pro Pro Asn Thr Thr Gly Glu Lys Cys Ser Glu Cys
025                1030                1035                1040

Leu Pro Asn Thr Trp Gly His Ser Ile Val Thr Gly Cys Lys Val Cys
                1045                1050                1055

Asn Cys Ser Thr Val Gly Ser Leu Ala Ser Gln Cys Asn Val Asn Thr
            1060                1065                1070

Gly Gln Cys Ser Cys His Pro Lys Phe Ser Gly Met Lys Cys Ser Glu
        1075                1080                1085

Cys Ser Arg Gly His Trp Asn Tyr Pro Leu Cys Thr Leu Cys Asp Cys
    1090                1095                1100

Phe Leu Pro Gly Thr Asp Ala Thr Thr Cys Asp Leu Glu Thr Arg Lys
105                1110                1115                1120

Cys Ser Cys Ser Asp Gln Thr Gly Gln Cys Ser Cys Lys Val Asn Val
                1125                1130                1135

Glu Gly Val His Cys Asp Arg Cys Arg Pro Gly Lys Phe Gly Leu Asp
            1140                1145                1150

Ala Lys Asn Pro Leu Gly Cys Ser Ser Cys Tyr Cys Phe Gly Val Thr
        1155                1160                1165

Ser Gln Cys Ser Glu Ala Lys Gly Leu Ile Arg Thr Trp Val Thr Leu
    1170                1175                1180
```

```
Ser Asp Glu Gln Thr Ile Leu Pro Leu Val Asp Glu Ala Leu Gln His
185                 1190                1195                1200

Thr Thr Thr Lys Gly Ile Ala Phe Gln Lys Pro Glu Ile Val Ala Lys
                1205                1210                1215

Met Asp Glu Val Arg Gln Glu Leu His Leu Glu Pro Phe Tyr Trp Lys
            1220                1225                1230

Leu Pro Gln Gln Phe Glu Gly Lys Lys Leu Met Ala Tyr Gly Gly Lys
        1235                1240                1245

Leu Lys Tyr Ala Ile Tyr Phe Glu Ala Arg Asp Glu Thr Gly Phe Ala
    1250                1255                1260

Thr Tyr Lys Pro Gln Val Ile Ile Arg Gly Gly Thr Pro Thr His Ala
265                 1270                1275                1280

Arg Ile Ile Thr Arg His Met Ala Ala Pro Leu Ile Gly Gln Leu Thr
                1285                1290                1295

Arg His Glu Ile Glu Met Thr Glu Lys Glu Trp Lys Tyr Tyr Gly Asp
            1300                1305                1310

Asp Pro Arg Ile Ser Arg Thr Val Thr Arg Glu Asp Phe Leu Asp Ile
        1315                1320                1325

Leu Tyr Asp Ile His Tyr Ile Leu Ile Lys Ala Thr Tyr Gly Asn Val
    1330                1335                1340

Val Arg Gln Ser Arg Ile Ser Glu Ile Ser Met Glu Val Ala Glu Pro
345                 1350                1355                1360

Gly His Val Leu Ala Gly Ser Pro Pro Ala His Leu Ile Glu Arg Cys
                1365                1370                1375

Asp Cys Pro Pro Gly Tyr Ser Gly Leu Ser Cys Glu Thr Cys Ala Pro
            1380                1385                1390

Gly Phe Tyr Arg Leu Arg Ser Glu Pro Gly Gly Arg Thr Pro Gly Pro
        1395                1400                1405

Thr Leu Gly Thr Cys Val Pro Cys Gln Cys Asn Gly His Ser Ser Gln
    1410                1415                1420

Cys Asp Pro Glu Thr Ser Val Cys Gln Asn Cys Gln His His Thr Ala
425                 1430                1435                1440

Gly Asp Phe Cys Glu Arg Cys Ala Leu Gly Tyr Tyr Gly Ile Val Arg
                1445                1450                1455

Gly Leu Pro Asn Asp Cys Gln Pro Cys Ala Cys Pro Leu Ile Ser Pro
            1460                1465                1470

Ser Asn Asn Phe Ser Pro Ser Cys Val Leu Glu Gly Leu Glu Asp Tyr
        1475                1480                1485

Arg Cys Thr Ala Cys Pro Arg Gly Tyr Glu Gly Gln Tyr Cys Glu Arg
    1490                1495                1500
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Cys Ala Pro Gly Tyr Thr Gly Ser Pro Ser Ser Pro Gly Gly Ser Cys
505                 1510                1515                1520

Gln Glu Cys Glu Cys Asp Pro Tyr Gly Ser Leu Pro Val Pro Cys Asp
            1525                1530                1535

Arg Val Thr Gly Leu Cys Thr Cys Arg Pro Gly Ala Thr Gly Arg Lys
        1540                1545                1550

Cys Asp Gly Cys Glu His Trp His Ala Arg Glu Gly Ala Glu Cys Val
    1555                1560                1565

Phe Cys Gly Asp Glu Cys Thr Gly Leu Leu Leu Gly Asp Leu Ala Arg
1570                1575                1580

Leu Glu Gln Met Thr Met Asn Ile Asn Leu Thr Gly Pro Leu Pro Ala
585                 1590                1595                1600

Pro Tyr Lys Ile Leu Tyr Gly Leu Glu Asn Thr Thr Gln Glu Leu Lys
            1605                1610                1615

His Leu Leu Ser Pro Gln Arg Ala Pro Glu Arg Leu Ile Gln Leu Ala
        1620                1625                1630

Glu Gly Asn Val Asn Thr Leu Val Met Glu Thr Asn Glu Leu Leu Thr
    1635                1640                1645

Arg Ala Thr Lys Val Thr Ala Asp Gly Glu Gln Thr Gly Gln Asp Ala
1650                1655                1660

Glu Arg Thr Asn Ser Arg Ala Glu Ser Leu Glu Glu Phe Ile Lys Gly
665                 1670                1675                1680

Leu Val Gln Asp Ala Glu Ala Ile Asn Glu Lys Ala Val Lys Leu Asn
            1685                1690                1695

Glu Thr Leu Gly Asn Gln Asp Lys Thr Ala Glu Arg Asn Leu Glu Glu
        1700                1705                1710

Leu Gln Lys Glu Ile Asp Arg Met Leu Lys Glu Leu Arg Ser Lys Asp
    1715                1720                1725

Leu Gln Thr Gln Lys Glu Val Ala Glu Asp Glu Leu Val Ala Ala Glu
1730                1735                1740

Gly Leu Leu Lys Arg Val Asn Lys Leu Phe Gly Glu Pro Arg Ala Gln
745                 1750                1755                1760

Asn Glu Asp Met Glu Lys Asp Leu Gln Gln Lys Leu Ala Glu Tyr Lys
            1765                1770                1775

Asn Lys Leu Asp Asp Ala Trp Asp Leu Leu Arg Glu Ala Thr Asp Lys
        1780                1785                1790

Thr Arg Asp Ala Asn Arg Leu Ser Ala Ala Asn Gln Lys Asn Met Thr
    1795                1800                1805

Ile Leu Glu Thr Lys Lys Glu Ala Ile Glu Gly Ser Lys Arg Gln Ile
1810                1815                1820

Glu Asn Thr Leu Lys Glu Gly Asn Asp Ile Leu Asp Glu Ala Asn Gln
```

825 1830 1835 1840

Leu Leu Gly Glu Ile Asn Ser Val Ile Asp Tyr Val Asp Asp Ile Lys
1845 1850 1855

Thr Lys Leu Pro Pro Met Ser Glu Glu Leu Ser Asp Lys Ile Asp Asp
1860 1865 1870

Leu Ala Gln Glu Ile Lys Asp Arg Arg Leu Ala Glu Lys Val Phe Gln
1875 1880 1885

Ala Glu Ser His Ala Ala Gln Leu Asn Asp Ser Ser Ala Val Leu Asp
1890 1895 1900

Gly Ile Leu Asp Glu Ala Lys Asn Ile Ser Phe Asn Ala Thr Ala Ala
905 1910 1915 1920

Phe Arg Ala Tyr Ser Asn Ile Lys Asp Tyr Ile Asp Glu Ala Glu Lys
1925 1930 1935

Val Ala Arg Glu Ala Lys Glu Leu Ala Gln Gly Ala Thr Lys Leu Ala
1940 1945 1950

Thr Ser Pro Gln Gly Leu Leu Lys Glu Asp Ala Lys Gly Ser Leu Gln
1955 1960 1965

Lys Ser Phe Arg Ile Leu Asn Glu Ala Lys Lys Leu Ala Asn Asp Val
1970 1975 1980

Lys Gly Asn His Asn Asp Leu Asn Asp Leu Lys Thr Arg Leu Glu Thr
985 1990 1995 2000

Ala Asp Leu Arg Asn Ser Gly Leu Leu Gly Ala Leu Asn Asp Thr Met
2005 2010 2015

Asp Lys Leu Ser Ala Ile Thr Asn Asp Thr Ala Ala Lys Leu Gln Ala
2020 2025 2030

Val Lys Glu Lys Ala Arg Glu Ala Asn Asp Thr Ala Lys Ala Val Leu
2035 2040 2045

Ala Gln Val Lys Asp Leu His Gln Asn Leu Asp Gly Leu Lys Gln Asn
2050 2055 2060

Tyr Asn Lys Leu Ala Asp Ser Val Ala Lys Thr Asn Ala Val Val Lys
065 2070 2075 2080

Asp Pro Ser Lys Asn Lys Ile Ile Ala Asp Ala Gly Thr Ser Val Arg
2085 2090 2095

Asn Leu Glu Gln Glu Ala Asp Arg Leu Ile Asp Lys Leu Lys Pro Ile
2100 2105 2110

Lys Glu Leu Glu Asp Asn Leu Lys Lys Asn Ile Ser Glu Ile Lys Glu
2115 2120 2125

Leu Ile Asn Gln Ala Arg Lys Gln Ala Asn Ser Ile Lys Val Ser Val
2130 2135 2140

Ser Ser Gly Gly Asp Cys Val Arg Thr Tyr Arg Pro Glu Ile Lys Lys
145 2150 2155 2160

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Gly Ser Tyr Asn Asn Ile Val Val His Val Lys Thr Ala Val Ala Asp
                2165                2170                2175

Asn Leu Leu Phe Tyr Leu Gly Ser Ala Lys Phe Ile Asp Phe Leu Ala
            2180                2185                2190

Ile Glu Met Arg Lys Gly Lys Val Ser Phe Leu Trp Ile Val Gly Ser
        2195                2200                2205

Gly Val Gly Arg Val Gly Phe Pro Asp Leu Thr Ile Asp Asp Ser Tyr
    2210                2215                2220

Trp Tyr Arg Ile Glu Ala Ser Arg Thr Gly Arg Asn Gly Ser Ile Ser
225                 2230                2235                2240

Val Arg Ala Leu Asp Gly Pro Lys Ala Ser Met Val Pro Ser Thr Tyr
                2245                2250                2255

His Ser Val Ser Pro Pro Gly Tyr Thr Ile Leu Asp Val Asp Ala Asn
            2260                2265                2270

Ala Met Leu Phe Val Gly Gly Leu Thr Gly Lys Ile Lys Lys Ala Asp
        2275                2280                2285

Ala Val Arg Val Ile Thr Phe Thr Gly Cys Met Gly Glu Thr Tyr Phe
    2290                2295                2300

Asp Asn Lys Pro Ile Gly Leu Trp Asn Phe Arg Glu Lys Glu Gly Asp
305                 2310                2315                2320

Cys Lys Gly Cys Thr Val Ser Pro Gln Val Glu Asp Ser Glu Gly Thr
                2325                2330                2335

Ile Gln Phe Asp Gly Glu Gly Tyr Ala Leu Val Ser Arg Pro Ile Arg
            2340                2345                2350

Trp Tyr Pro Asn Ile Ser Thr Val Met Phe Lys Phe Arg Thr Phe Ser
        2355                2360                2365

Ser Ser Ala Leu Leu Met Tyr Leu Ala Thr Arg Asp Leu Lys Asp Phe
    2370                2375                2380

Met Ser Val Glu Leu Ser Asp Gly His Val Lys Val Ser Tyr Asp Leu
385                 2390                2395                2400

Gly Ser Gly Met Thr Ser Val Val Ser Asn Gln Asn His Asn Asp Gly
                2405                2410                2415

Lys Trp Lys Ala Phe Thr Leu Ser Arg Ile Gln Lys Gln Ala Asn Ile
            2420                2425                2430

Ser Ile Val Asp Ile Asp Ser Asn Gln Glu Glu Asn Val Ala Thr Ser
        2435                2440                2445

Ser Ser Gly Asn Asn Phe Gly Leu Asp Leu Lys Ala Asp Asp Lys Ile
    2450                2455                2460

Tyr Phe Gly Gly Leu Pro Thr Leu Arg Asn Leu Ser Met Lys Ala Arg
465                 2470                2475                2480
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Pro Glu Val Asn Val Lys Lys Tyr Ser Gly Cys Leu Lys Asp Ile Glu
                2485                2490                2495

Ile Ser Arg Thr Pro Tyr Asn Ile Leu Ser Ser Pro Asp Tyr Val Gly
            2500                2505                2510

Val Thr Lys Gly Cys Ser Leu Glu Asn Val Asn Thr Val Ser Phe Pro
        2515                2520                2525

Lys Pro Gly Phe Val Glu Leu Ala Ala Val Ser Ile Asp Val Gly Thr
    2530                2535                2540

Glu Ile Asn Leu Ser Phe Ser Thr Arg Asn Glu Ser Gly Ile Ile Leu
545                 2550                2555                2560

Leu Gly Ser Gly Gly Thr Leu Thr Pro Pro Arg Arg Lys Arg Arg Gln
                2565                2570                2575

Thr Thr Gln Ala Tyr Tyr Ala Ile Phe Leu Asn Lys Gly Arg Leu Glu
            2580                2585                2590

Val His Leu Ser Ser Gly Thr Arg Thr Met Arg Lys Ile Val Ile Lys
        2595                2600                2605

Pro Glu Pro Asn Leu Phe His Asp Gly Arg Glu His Ser Val His Val
    2610                2615                2620

Glu Arg Thr Arg Gly Ile Phe Thr Val Gln Ile Asp Glu Asp Arg Arg
625                 2630                2635                2640

His Ile Gln Asn Leu Thr Glu Glu Gln Pro Ile Glu Val Lys Lys Leu
                2645                2650                2655

Phe Val Gly Gly Ala Pro Pro Glu Phe Gln Pro Ser Pro Leu Arg Asn
            2660                2665                2670

Ile Pro Ala Phe Gln Gly Cys Val Trp Asn Leu Val Ile Asn Ser Ile
        2675                2680                2685

Pro Met Asp Phe Ala Gln Pro Ile Ala Phe Lys Asn Ala Asp Ile Gly
    2690                2695                2700

Arg Cys Thr Tyr Gln Lys Pro Arg Glu Asp Glu Ser Glu Ala Val Pro
705                 2710                2715                2720

Ala Glu Val Ile Val Gln Pro Gln Ser Val Pro Thr Pro Ala Phe Pro
                2725                2730                2735

Phe Pro Val Pro Thr Met Val His Gly Pro Cys Val Ala Glu Ser Glu
            2740                2745                2750

Pro Ala Leu Leu Thr Gly Ser Lys Gln Phe Gly Leu Ser Arg Asn Ser
        2755                2760                2765

His Ile Ala Ile Val Phe Asp Asp Thr Lys Val Lys Asn Arg Leu Thr
    2770                2775                2780

Ile Glu Leu Glu Val Arg Thr Glu Ala Glu Ser Gly Leu Leu Phe Tyr
785                 2790                2795                2800

Met Gly Arg Ile Asn His Ala Asp Phe Gly Thr Val Gln Leu Arg Asn
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2805 2810 2815

Gly Phe Pro Phe Phe Ser Tyr Asp Leu Gly Ser Gly Ser Thr Arg Thr
2820 2825 2830

Met Ile Pro Thr Lys Ile Asn Asp Gly Gln Trp His Lys Ile Lys Ile
2835 2840 2845

Val Arg Val Lys Gln Glu Gly Ile Leu Tyr Val Asp Asp Ala Ser Ser
2850 2855 2860

Gln Thr Ile Ser Pro Lys Lys Ala Asp Ile Leu Asp Val Gly Gly Ile
865 2870 2875 2880

Leu Tyr Val Gly Gly Leu Pro Ile Asn Tyr Thr Thr Arg Arg Ile Gly
2885 2890 2895

Pro Val Thr Tyr Ser Leu Asp Gly Cys Val Arg Asn Leu His Met Glu
2900 2905 2910

Gln Ala Pro Val Asp Leu Asp Gln Pro Thr Ser Ser Phe His Val Gly
2915 2920 2925

Thr Cys Phe Ala Asn Ala Glu Ser Gly Thr Tyr Phe Asp Gly Thr Gly
2930 2935 2940

Phe Gly Lys Ala Val Gly Gly Phe Ile Val Gly Leu Asp Leu Leu Val
945 2950 2955 2960

Glu Phe Glu Phe Arg Thr Thr Arg Pro Thr Gly Val Leu Leu Gly Ile
2965 2970 2975

Ser Ser Gln Lys Met Asp Gly Met Gly Ile Glu Met Ile Asp Glu Lys
2980 2985 2990

Leu Met Phe His Val Asp Asn Gly Ala Gly Arg Phe Thr Ala Ile Tyr
2995 3000 3005

Asp Ala Glu Ile Pro Gly His Met Cys Asn Gly Gln Trp Tyr Lys Val
3010 3015 3020

Thr Ala Lys Lys Ile Lys Asn Arg Leu Glu Leu Val Val Asp Gly Asn
025 3030 3035 3040

Gln Val Asp Ala Gln Ser Pro Asn Ser Ala Ser Thr Ser Ala Asp Thr
3045 3050 3055

Asn Asp Pro Val Phe Val Gly Gly Phe Pro Gly Gly Leu Asn Gln Phe
3060 3065 3070

Gly Leu Thr Thr Asn Ile Arg Phe Arg Gly Cys Ile Arg Ser Leu Lys
3075 3080 3085

Leu Thr Lys Gly Thr Ala Asn Arg Trp Arg Leu Ile Leu Pro Arg Pro
3090 3095 3100

Trp Asn
105

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Gln Arg Arg Gln Ser Gln Ala His Gln Gln Arg Gly Leu Phe Pro Ala
  1               5                  10                  15

gtc ctg aat ctt gct tcg aat gca ctc atc aca acc aat gct aca tgt   96
Val Leu Asn Leu Ala Ser Asn Ala Leu Ile Thr Thr Asn Ala Thr Cys
             20                  25                  30

ggg gaa aaa gga ccc gag atg tac tgc aag ttg gtg gaa cat gtc ccc   144
Gly Glu Lys Gly Pro Glu Met Tyr Cys Lys Leu Val Glu His Val Pro
         35                  40                  45

ggg cag cct gtg agg aac cct cag tgc cga atc tgc aat cag aac agc   192
Gly Gln Pro Val Arg Asn Pro Gln Cys Arg Ile Cys Asn Gln Asn Ser
     50                  55                  60

agc aat cca tac cag agg cac ccg att acg aat gct att gat ggc aag   240
Ser Asn Pro Tyr Gln Arg His Pro Ile Thr Asn Ala Ile Asp Gly Lys
 65                  70                  75                  80

aac aca tgg tgg cag agt ccc agt atc aag aat gga gtg gaa tac cat   288
Asn Thr Trp Trp Gln Ser Pro Ser Ile Lys Asn Gly Val Glu Tyr His
                 85                  90                  95

tat gtg aca att act ctg gat tta cag cag gtg ttc cag att gcc tac   336
Tyr Val Thr Ile Thr Leu Asp Leu Gln Gln Val Phe Gln Ile Ala Tyr
            100                 105                 110

gta att gtg aag gca gcc aat tcc cct cgg cct gga aac tgg att ttg   384
Val Ile Val Lys Ala Ala Asn Ser Pro Arg Pro Gly Asn Trp Ile Leu
        115                 120                 125

gaa cgt tcc ctg gat gac gtg gag tac aaa ccc tgg cag tat cat gcg   432
Glu Arg Ser Leu Asp Asp Val Glu Tyr Lys Pro Trp Gln Tyr His Ala
    130                 135                 140

gtg aca gac acg gag tgc ctg acc ctc tac aat atc tat ccc cgc act   480
Val Thr Asp Thr Glu Cys Leu Thr Leu Tyr Asn Ile Tyr Pro Arg Thr
145                 150                 155                 160

gga cca cca tcc tac gcc aaa gat gat gag gtc atc tgc act tca ttt   528
Gly Pro Pro Ser Tyr Ala Lys Asp Asp Glu Val Ile Cys Thr Ser Phe
                165                 170                 175

tat tcg aag atc cac cct tta gaa aat gga gag att cac att tct ttg   576
Tyr Ser Lys Ile His Pro Leu Glu Asn Gly Glu Ile His Ile Ser Leu
            180                 185                 190

atc aat ggg aga cca agt gct gat gac ccc tcc cct gaa ctc ctg gaa   624
Ile Asn Gly Arg Pro Ser Ala Asp Asp Pro Ser Pro Glu Leu Leu Glu
        195                 200                 205
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```
ttc acc tct gct cgc tac att cgc ctg aga ttt cag agg atc cgc acc   672
Phe Thr Ser Ala Arg Tyr Ile Arg Leu Arg Phe Gln Arg Ile Arg Thr
    210                 215                 220

ttg aat gca gac ttg atg atg ttt gct cac aaa gac ccc aga gaa atc   720
Leu Asn Ala Asp Leu Met Met Phe Ala His Lys Asp Pro Arg Glu Ile
225                 230                 235                 240

gat ccc att gtc aca cga aga tat tac tat tct gtc aag gat att tca   768
Asp Pro Ile Val Thr Arg Arg Tyr Tyr Tyr Ser Val Lys Asp Ile Ser
                245                 250                 255

gtt ggc ggg atg tgc atc tgt tat ggt cat gcc cgg gct tgt cca ctt   816
Val Gly Gly Met Cys Ile Cys Tyr Gly His Ala Arg Ala Cys Pro Leu
            260                 265                 270

gac cct gca aca aat aaa tca cgc tgt gag tgt gaa cat aac acc tgt   864
Asp Pro Ala Thr Asn Lys Ser Arg Cys Glu Cys Glu His Asn Thr Cys
        275                 280                 285

ggg gaa agc tgt gac agg tgc tgt cca gga ttc cat cag aag cct tgg   912
Gly Glu Ser Cys Asp Arg Cys Cys Pro Gly Phe His Gln Lys Pro Trp
    290                 295                 300

aga gct gga acc ttc ctc acc aag tct gag tgt gaa gca tgc aat tgt   960
Arg Ala Gly Thr Phe Leu Thr Lys Ser Glu Cys Glu Ala Cys Asn Cys
305                 310                 315                 320

cac gga aaa gct gag gaa tgc tat tat gat gaa act gtt gct agc aga   1008
His Gly Lys Ala Glu Glu Cys Tyr Tyr Asp Glu Thr Val Ala Ser Arg
                325                 330                 335

aat cta agt tta aat ata cat ggg aag tac atc gga ggg ggt gtg tgc   1056
Asn Leu Ser Leu Asn Ile His Gly Lys Tyr Ile Gly Gly Gly Val Cys
            340                 345                 350

atc aac tgc aca cat aac acg gct ggg ata aat tgt gag aca tgt gtt   1104
Ile Asn Cys Thr His Asn Thr Ala Gly Ile Asn Cys Glu Thr Cys Val
        355                 360                 365

gat gga ttc ttc aga ccc aaa ggg gtg tca cca aat tat cca aga cca   1152
Asp Gly Phe Phe Arg Pro Lys Gly Val Ser Pro Asn Tyr Pro Arg Pro
    370                 375                 380

tgc cag cca tgt cac tgt gat cca act ggc tcc ctt agt gaa gtc tgt   1200
Cys Gln Pro Cys His Cys Asp Pro Thr Gly Ser Leu Ser Glu Val Cys
385                 390                 395                 400

gtc aaa gat gag aaa tac gcc cag cga ggg ttg aaa cct gga tcc tgt   1248
Val Lys Asp Glu Lys Tyr Ala Gln Arg Gly Leu Lys Pro Gly Ser Cys
                405                 410                 415

cac tgc aaa act ggc ttt gga ggc gtg aac tgt gat cgc tgt gtc agg   1296
His Cys Lys Thr Gly Phe Gly Gly Val Asn Cys Asp Arg Cys Val Arg
            420                 425                 430

ggt tac cat ggt tac cca gac tgc caa ccc tgt aac tgt agt ggc ttg   1344
Gly Tyr His Gly Tyr Pro Asp Cys Gln Pro Cys Asn Cys Ser Gly Leu
        435                 440                 445

ggg agc aca aat gag gac cct tgc gtt ggg ccc tgt agc tgt aag gag   1392
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Gly Ser Thr Asn Glu Asp Pro Cys Val Gly Pro Cys Ser Cys Lys Glu
    450                 455                 460

aat gtt gaa ggt gaa gac tgt agt cgt tgc aaa tct ggt ttc ttc aac   1440
Asn Val Glu Gly Glu Asp Cys Ser Arg Cys Lys Ser Gly Phe Phe Asn
465                 470                 475                 480

ttg caa gaa gat aat cag aaa ggc tgt gag gag tgt ttc tgt tca gga   1488
Leu Gln Glu Asp Asn Gln Lys Gly Cys Glu Glu Cys Phe Cys Ser Gly
                485                 490                 495

gta tca aac aga tgt cag agt tcc tac tgg acc tat ggg aat att caa   1536
Val Ser Asn Arg Cys Gln Ser Ser Tyr Trp Thr Tyr Gly Asn Ile Gln
            500                 505                 510

gac atg cgt ggt tgg tat ctc aca gac ctc tct ggc cgc att cgg atg   1584
Asp Met Arg Gly Trp Tyr Leu Thr Asp Leu Ser Gly Arg Ile Arg Met
        515                 520                 525

gct ccc cag ctt gat aac cct gac tca cct cag cag atc agc atc agt   1632
Ala Pro Gln Leu Asp Asn Pro Asp Ser Pro Gln Gln Ile Ser Ile Ser
    530                 535                 540

aac tct gag gcc cgg aaa tcc ctg ctt gat ggt tac tac tgg agt gca   1680
Asn Ser Glu Ala Arg Lys Ser Leu Leu Asp Gly Tyr Tyr Trp Ser Ala
545                 550                 555                 560

ccg cct cca tat ctg gga aac aga ctt cca gct gtt ggg gga cag ttg   1728
Pro Pro Pro Tyr Leu Gly Asn Arg Leu Pro Ala Val Gly Gly Gln Leu
                565                 570                 575

tca ttt acc atc tca tat gac ctc gaa gaa gag gaa gac gat aca gaa   1776
Ser Phe Thr Ile Ser Tyr Asp Leu Glu Glu Glu Glu Asp Asp Thr Glu
            580                 585                 590

aaa ctc ctt cag ctg atg att atc ttt gag gga aat gac tta aga atc   1824
Lys Leu Leu Gln Leu Met Ile Ile Phe Glu Gly Asn Asp Leu Arg Ile
        595                 600                 605

agc aca gcg tat aag gag gtg tac tta gag cca tct gaa gaa cac gtt   1872
Ser Thr Ala Tyr Lys Glu Val Tyr Leu Glu Pro Ser Glu Glu His Val
    610                 615                 620

gag gag gtg tca ctc aaa gaa gag gcc ttt act ata cat gga aca aat   1920
Glu Glu Val Ser Leu Lys Glu Glu Ala Phe Thr Ile His Gly Thr Asn
625                 630                 635                 640

ttg cca gtc act aga aaa gat ttc atg att gtt ctc aca aat ttg gga   1968
Leu Pro Val Thr Arg Lys Asp Phe Met Ile Val Leu Thr Asn Leu Gly
                645                 650                 655

gag atc ctt atc caa atc aca tac aac tta ggg atg gac gcc atc ttc   2016
Glu Ile Leu Ile Gln Ile Thr Tyr Asn Leu Gly Met Asp Ala Ile Phe
            660                 665                 670

agg ctg agt tct gtc aat ctt gaa tct cct gtc cct tat cct act gat   2064
Arg Leu Ser Ser Val Asn Leu Glu Ser Pro Val Pro Tyr Pro Thr Asp
        675                 680                 685

aga cgt att gca act gat gtg gaa gtt tgc cag tgt cca cct ggg tac   2112
Arg Arg Ile Ala Thr Asp Val Glu Val Cys Gln Cys Pro Pro Gly Tyr
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    690                 695                 700

agt ggc agc tct tgt gaa aca tgt tgg cct agg cac cga aga gtt aac   2160
Ser Gly Ser Ser Cys Glu Thr Cys Trp Pro Arg His Arg Arg Val Asn
705                 710                 715                 720

ggc acc att ttt ggt ggc att tgt gaa cca tgt cag tgc ttt gct cat   2208
Gly Thr Ile Phe Gly Gly Ile Cys Glu Pro Cys Gln Cys Phe Ala His
                725                 730                 735

gca gaa gcc tgt gat gac atc aca gga gaa tgt ctg aac tgt aag gat   2256
Ala Glu Ala Cys Asp Asp Ile Thr Gly Glu Cys Leu Asn Cys Lys Asp
            740                 745                 750

cac aca ggt ggg ccg tac tgc aat gaa tgt ctc cct gga ttc tat ggt   2304
His Thr Gly Gly Pro Tyr Cys Asn Glu Cys Leu Pro Gly Phe Tyr Gly
        755                 760                 765

gat cct act cga gga agc cct gaa gac tgt cag ccc tgt gcc tgt cca   2352
Asp Pro Thr Arg Gly Ser Pro Glu Asp Cys Gln Pro Cys Ala Cys Pro
    770                 775                 780

ctc aat atc cca tca aat aac ttt agt cca aca tgc cat tta gac cgg   2400
Leu Asn Ile Pro Ser Asn Asn Phe Ser Pro Thr Cys His Leu Asp Arg
785                 790                 795                 800

agt ctg gga ttg atc tgt gac gag tgt cct att ggg tac aca gga ccg   2448
Ser Leu Gly Leu Ile Cys Asp Glu Cys Pro Ile Gly Tyr Thr Gly Pro
                805                 810                 815

cgc tgt gag agg tgt gca gaa ggc tat ttt gga caa cct tcc gta cct   2496
Arg Cys Glu Arg Cys Ala Glu Gly Tyr Phe Gly Gln Pro Ser Val Pro
            820                 825                 830

gga gga tca tgt cag cca tgc caa tgc aat gac aac ctt gac tac tcc   2544
Gly Gly Ser Cys Gln Pro Cys Gln Cys Asn Asp Asn Leu Asp Tyr Ser
        835                 840                 845

atc cct ggc agc tgt gac agc ctg tct ggc tcc tgt ctg att tgt aag   2592
Ile Pro Gly Ser Cys Asp Ser Leu Ser Gly Ser Cys Leu Ile Cys Lys
    850                 855                 860

cca ggt aca aca ggc cgg tac tgt gag ctc tgt gct gat ggg tat ttt   2640
Pro Gly Thr Thr Gly Arg Tyr Cys Glu Leu Cys Ala Asp Gly Tyr Phe
865                 870                 875                 880

gga gac gcg gtt aat aca aag aac tgt caa cca tgc cgt tgt gat atc   2688
Gly Asp Ala Val Asn Thr Lys Asn Cys Gln Pro Cys Arg Cys Asp Ile
                885                 890                 895

aat ggc tcc ttc tca gag gat tgt cac aca aga act ggg caa tgt gag   2736
Asn Gly Ser Phe Ser Glu Asp Cys His Thr Arg Thr Gly Gln Cys Glu
            900                 905                 910

tgc aga ccc aat gtt cag ggg cgg cac tgt gac gag tgt aag cct gaa   2784
Cys Arg Pro Asn Val Gln Gly Arg His Cys Asp Glu Cys Lys Pro Glu
        915                 920                 925

acc ttt ggc ctg caa ctg gga agg ggt tgt ctg ccc tgc aac tgc aat   2832
Thr Phe Gly Leu Gln Leu Gly Arg Gly Cys Leu Pro Cys Asn Cys Asn
    930                 935                 940
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tct ttt ggg tct aag tcc ttt gac tgt gaa gca agt ggg cag tgc tgg   2880
Ser Phe Gly Ser Lys Ser Phe Asp Cys Glu Ala Ser Gly Gln Cys Trp
945                 950                 955                 960

tgc cag cct gga gta gca ggg aag aaa tgt gac cgt tgt gcc cat ggc   2928
Cys Gln Pro Gly Val Ala Gly Lys Lys Cys Asp Arg Cys Ala His Gly
                965                 970                 975

tac ttc aac ttc caa gaa gga ggc tgc ata gct tgt gac tgt tct cat   2976
Tyr Phe Asn Phe Gln Glu Gly Gly Cys Ile Ala Cys Asp Cys Ser His
            980                 985                 990

ctg ggc aac aac tgt gac cca aaa act ggc caa tgc att tgc cca ccc   3024
Leu Gly Asn Asn Cys Asp Pro Lys Thr Gly Gln Cys Ile Cys Pro Pro
        995                1000                1005

aat acc act gga gaa aag tgt tct gag tgt ctt ccc aac acc tgg ggt   3072
Asn Thr Thr Gly Glu Lys Cys Ser Glu Cys Leu Pro Asn Thr Trp Gly
    1010                1015                1020

cac agc att gtc acc ggc tgt aag gtt tgt aac tgc agc act gtg ggg   3120
His Ser Ile Val Thr Gly Cys Lys Val Cys Asn Cys Ser Thr Val Gly
1025                1030                1035                1040

tcc ttg gct tct cag tgc aat gta aac acg ggc cag tgc agc tgt cat   3168
Ser Leu Ala Ser Gln Cys Asn Val Asn Thr Gly Gln Cys Ser Cys His
                1045                1050                1055

cca aaa ttc tct ggt atg aaa tgc tca gag tgc agc cga ggt cac tgg   3216
Pro Lys Phe Ser Gly Met Lys Cys Ser Glu Cys Ser Arg Gly His Trp
            1060                1065                1070

aac tat cct ctc tgc act cta tgt gac tgc ttc ctt cca ggc aca gat   3264
Asn Tyr Pro Leu Cys Thr Leu Cys Asp Cys Phe Leu Pro Gly Thr Asp
        1075                1080                1085

gcc acg act tgt gat ctg gag act agg aaa tgc tcc tgt agt gat caa   3312
Ala Thr Thr Cys Asp Leu Glu Thr Arg Lys Cys Ser Cys Ser Asp Gln
    1090                1095                1100

act gga cag tgc agc tgt aag gtg aat gtg gaa ggc gtc cac tgt gac   3360
Thr Gly Gln Cys Ser Cys Lys Val Asn Val Glu Gly Val His Cys Asp
1105                1110                1115                1120

agg tgc cgg cct ggc aaa ttt gga cta gat gcc aag aac cca ctt ggc   3408
Arg Cys Arg Pro Gly Lys Phe Gly Leu Asp Ala Lys Asn Pro Leu Gly
                1125                1130                1135

tgc agc agc tgc tac tgc ttt gga gtt act agt caa tgc tct gaa gca   3456
Cys Ser Ser Cys Tyr Cys Phe Gly Val Thr Ser Gln Cys Ser Glu Ala
            1140                1145                1150

aag ggg ctg atc cgt acg tgg gtg act ttg agt gat gaa cag acc att   3504
Lys Gly Leu Ile Arg Thr Trp Val Thr Leu Ser Asp Glu Gln Thr Ile
        1155                1160                1165

cta cct ctg gtg gat gag gcc ctg cag cac acg act acc aaa ggc att   3552
Leu Pro Leu Val Asp Glu Ala Leu Gln His Thr Thr Thr Lys Gly Ile
    1170                1175                1180
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gct ttc cag aaa cca gag att gtt gca aag atg gat gaa gtc agg caa   3600
Ala Phe Gln Lys Pro Glu Ile Val Ala Lys Met Asp Glu Val Arg Gln
1185               1190                1195                1200

gag ctc cat ttg gaa cct ttt tac tgg aaa ctc cca caa caa ttt gaa   3648
Glu Leu His Leu Glu Pro Phe Tyr Trp Lys Leu Pro Gln Gln Phe Glu
              1205                1210                1215

ggg aaa aag ttg atg gct tat ggt ggc aaa ctc aag tat gcc atc tat   3696
Gly Lys Lys Leu Met Ala Tyr Gly Gly Lys Leu Lys Tyr Ala Ile Tyr
          1220                1225                1230

ttt gag gct cgg gat gag aca ggc ttt gcc aca tat aaa cct caa gtt   3744
Phe Glu Ala Arg Asp Glu Thr Gly Phe Ala Thr Tyr Lys Pro Gln Val
      1235                1240                1245

atc att cga ggt gga act cct act cat gct aga att att acc aga cac   3792
Ile Ile Arg Gly Gly Thr Pro Thr His Ala Arg Ile Ile Thr Arg His
  1250                1255                1260

atg gct gcc cct ctc att ggc cag ttg aca cgg cat gaa ata gaa atg   3840
Met Ala Ala Pro Leu Ile Gly Gln Leu Thr Arg His Glu Ile Glu Met
1265               1270                1275                1280

aca gag aaa gaa tgg aaa tat tat ggt gat gat cct cga atc agt aga   3888
Thr Glu Lys Glu Trp Lys Tyr Tyr Gly Asp Asp Pro Arg Ile Ser Arg
              1285                1290                1295

act gtg acc cgt gaa gac ttc ttg gat ata cta tat gat att cac tat   3936
Thr Val Thr Arg Glu Asp Phe Leu Asp Ile Leu Tyr Asp Ile His Tyr
          1300                1305                1310

atc ctt atc aag gct act tat gga aac gtt gtg aga caa agc cgc att   3984
Ile Leu Ile Lys Ala Thr Tyr Gly Asn Val Val Arg Gln Ser Arg Ile
      1315                1320                1325

tct gaa atc tcc atg gaa gta gct gaa cca gga cat gta tta gca ggg   4032
Ser Glu Ile Ser Met Glu Val Ala Glu Pro Gly His Val Leu Ala Gly
  1330                1335                1340

agc cca cca gca cac ttg ata gaa aga tgc gat tgc cct cct ggc tat   4080
Ser Pro Pro Ala His Leu Ile Glu Arg Cys Asp Cys Pro Pro Gly Tyr
1345               1350                1355                1360

tct ggc ttg tct tgt gag acg tgt gca cca gga ttt tac cga ctt cgt   4128
Ser Gly Leu Ser Cys Glu Thr Cys Ala Pro Gly Phe Tyr Arg Leu Arg
              1365                1370                1375

tct gaa cca ggt ggg cgg act cct gga cca acc tta ggg acc tgt gtt   4176
Ser Glu Pro Gly Gly Arg Thr Pro Gly Pro Thr Leu Gly Thr Cys Val
          1380                1385                1390

ccc tgc caa tgt aat gga cac agc agt cag tgt gat cct gag acc tca   4224
Pro Cys Gln Cys Asn Gly His Ser Ser Gln Cys Asp Pro Glu Thr Ser
      1395                1400                1405

gta tgc cag aat tgt cag cat cac act gct ggt gac ttc tgt gag cgc   4272
Val Cys Gln Asn Cys Gln His His Thr Ala Gly Asp Phe Cys Glu Arg
  1410                1415                1420

tgt gcc ctt ggc tac tat gga atc gtc agg gga ttg cca aat gac tgc   4320
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Cys Ala Leu Gly Tyr Tyr Gly Ile Val Arg Gly Leu Pro Asn Asp Cys
1425                1430                1435                1440

caa cca tgt gct tgt cct ctg att tcg ccc agc aac aat ttc agc ccc   4368
Gln Pro Cys Ala Cys Pro Leu Ile Ser Pro Ser Asn Asn Phe Ser Pro
                1445                1450                1455

tct tgt gta ttg gaa ggt ctg gaa gat tac cgt tgc acc gcc tgc cca   4416
Ser Cys Val Leu Glu Gly Leu Glu Asp Tyr Arg Cys Thr Ala Cys Pro
            1460                1465                1470

agg ggc tat gaa gga cag tac tgt gaa agg tgt gcc cca ggc tat act   4464
Arg Gly Tyr Glu Gly Gln Tyr Cys Glu Arg Cys Ala Pro Gly Tyr Thr
        1475                1480                1485

ggc agc cca agc agc ccc gga ggc tcc tgc caa gaa tgt gag tgt gac   4512
Gly Ser Pro Ser Ser Pro Gly Gly Ser Cys Gln Glu Cys Glu Cys Asp
    1490                1495                1500

cct tat ggc tcc cta ccg gtt ccc tgt gac cgg gtc aca gga ctc tgc   4560
Pro Tyr Gly Ser Leu Pro Val Pro Cys Asp Arg Val Thr Gly Leu Cys
1505                1510                1515                1520

acg tgc cgc cct gga gcc aca gga agg aag tgt gat ggc tgc gag cac   4608
Thr Cys Arg Pro Gly Ala Thr Gly Arg Lys Cys Asp Gly Cys Glu His
                1525                1530                1535

tgg cat gca cgc gag ggt gca gag tgt gtc ttt tgt gga gac gag tgt   4656
Trp His Ala Arg Glu Gly Ala Glu Cys Val Phe Cys Gly Asp Glu Cys
            1540                1545                1550

aca ggc ctt ctt ctt ggt gac ctg gct cgt cta gag cag atg acc atg   4704
Thr Gly Leu Leu Leu Gly Asp Leu Ala Arg Leu Glu Gln Met Thr Met
        1555                1560                1565

aac atc aac ctc acg ggc cca ctg cct gct cca tat aaa att ctg tat   4752
Asn Ile Asn Leu Thr Gly Pro Leu Pro Ala Pro Tyr Lys Ile Leu Tyr
    1570                1575                1580

ggt ctt gaa aat aca act cag gaa ctc aag cac ctg cta tca ccg caa   4800
Gly Leu Glu Asn Thr Thr Gln Glu Leu Lys His Leu Leu Ser Pro Gln
1585                1590                1595                1600

cgg gca cca gag agg ctc att cag ttg gca gag ggc aac gtg aac aca   4848
Arg Ala Pro Glu Arg Leu Ile Gln Leu Ala Glu Gly Asn Val Asn Thr
                1605                1610                1615

ctt gtg atg gaa aca aat gag ctg cta acc aga gca acc aaa gtg aca   4896
Leu Val Met Glu Thr Asn Glu Leu Leu Thr Arg Ala Thr Lys Val Thr
            1620                1625                1630

gca gat ggt gag caa aca gga caa gat gct gag agg acc aac tcc aga   4944
Ala Asp Gly Glu Gln Thr Gly Gln Asp Ala Glu Arg Thr Asn Ser Arg
        1635                1640                1645

gca gaa tcc ttg gaa gaa ttc att aaa ggg ctt gtc cag gat gct gaa   4992
Ala Glu Ser Leu Glu Glu Phe Ile Lys Gly Leu Val Gln Asp Ala Glu
    1650                1655                1660

gcc ata aat gaa aaa gct gta aaa cta aat gaa acc tta gga aat caa   5040
Ala Ile Asn Glu Lys Ala Val Lys Leu Asn Glu Thr Leu Gly Asn Gln
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1665                1670                1675                1680

gat aag aca gca gag aga aac ttg gag gag ctt caa aag gaa atc gac   5088
Asp Lys Thr Ala Glu Arg Asn Leu Glu Glu Leu Gln Lys Glu Ile Asp
                1685                1690                1695

cgg atg ctg aag gaa ctg aga agt aaa gat ctt caa aca cag aag gaa   5136
Arg Met Leu Lys Glu Leu Arg Ser Lys Asp Leu Gln Thr Gln Lys Glu
            1700                1705                1710

gtt gct gag gat gag ctc gtg gca gca gaa ggc ctt ctg aag aga gta   5184
Val Ala Glu Asp Glu Leu Val Ala Ala Glu Gly Leu Leu Lys Arg Val
        1715                1720                1725

aac aag ctg ttt gga gag ccc aga gcc cag aat gaa gat atg gaa aag   5232
Asn Lys Leu Phe Gly Glu Pro Arg Ala Gln Asn Glu Asp Met Glu Lys
    1730                1735                1740

gat ctc cag cag aaa ctg gca gag tac aag aac aaa ctt gat gat gct   5280
Asp Leu Gln Gln Lys Leu Ala Glu Tyr Lys Asn Lys Leu Asp Asp Ala
1745                1750                1755                1760

tgg gat cta ttg aga gaa gcc act gat aaa acc cga gat gct aat cgt   5328
Trp Asp Leu Leu Arg Glu Ala Thr Asp Lys Thr Arg Asp Ala Asn Arg
                1765                1770                1775

ttg tct gct gcc aat caa aaa aac atg acc ata ctg gag aca aag aag   5376
Leu Ser Ala Ala Asn Gln Lys Asn Met Thr Ile Leu Glu Thr Lys Lys
            1780                1785                1790

gag gct att gaa ggt agc aaa cga caa ata gag aac act tta aag gaa   5424
Glu Ala Ile Glu Gly Ser Lys Arg Gln Ile Glu Asn Thr Leu Lys Glu
        1795                1800                1805

ggc aat gac atc ctt gat gaa gcc aat caa ctc tta ggt gaa atc aac   5472
Gly Asn Asp Ile Leu Asp Glu Ala Asn Gln Leu Leu Gly Glu Ile Asn
    1810                1815                1820

tca gtc ata gat tat gtc gac gac att aaa act aag ttg cca cca atg   5520
Ser Val Ile Asp Tyr Val Asp Asp Ile Lys Thr Lys Leu Pro Pro Met
1825                1830                1835                1840

tcc gag gag ctg agt gac aaa ata gat gac ctc gcc cag gaa ata aag   5568
Ser Glu Glu Leu Ser Asp Lys Ile Asp Asp Leu Ala Gln Glu Ile Lys
                1845                1850                1855

gac aga agg ctt gct gag aag gtg ttc cag gct gag agc cat gct gct   5616
Asp Arg Arg Leu Ala Glu Lys Val Phe Gln Ala Glu Ser His Ala Ala
            1860                1865                1870

cag ctg aac gac tcg tct gct gta ctt gat gga atc ctg gat gag gct   5664
Gln Leu Asn Asp Ser Ser Ala Val Leu Asp Gly Ile Leu Asp Glu Ala
        1875                1880                1885

aag aac atc tct ttc aat gcc acg gca gcc ttc aga gct tac agt aat   5712
Lys Asn Ile Ser Phe Asn Ala Thr Ala Ala Phe Arg Ala Tyr Ser Asn
    1890                1895                1900

att aaa gac tac att gat gaa gct gag aaa gtg gcc aga gaa gcc aaa   5760
Ile Lys Asp Tyr Ile Asp Glu Ala Glu Lys Val Ala Arg Glu Ala Lys
1905                1910                1915                1920
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gag ctt gcc caa ggg gct aca aaa ctg gca aca agt cct cag ggc tta   5808
Glu Leu Ala Gln Gly Ala Thr Lys Leu Ala Thr Ser Pro Gln Gly Leu
                1925                1930                1935

tta aaa gaa gat gcc aaa ggc tcc ctt cag aaa agc ttc agg atc ctc   5856
Leu Lys Glu Asp Ala Lys Gly Ser Leu Gln Lys Ser Phe Arg Ile Leu
            1940                1945                1950

aat gaa gcc aag aag cta gca aac gat gtg aaa gga aat cac aat gat   5904
Asn Glu Ala Lys Lys Leu Ala Asn Asp Val Lys Gly Asn His Asn Asp
        1955                1960                1965

cta aat gac ctg aaa acc agg tta gaa act gct gac ctt aga aac agt   5952
Leu Asn Asp Leu Lys Thr Arg Leu Glu Thr Ala Asp Leu Arg Asn Ser
    1970                1975                1980

gga ctt cta gga gct cta aat gac acc atg gac aag tta tca gcc att   6000
Gly Leu Leu Gly Ala Leu Asn Asp Thr Met Asp Lys Leu Ser Ala Ile
1985                1990                1995                2000

aca aat gac acg gct gct aaa ctg cag gct gtc aaa gag aaa gcc aga   6048
Thr Asn Asp Thr Ala Ala Lys Leu Gln Ala Val Lys Glu Lys Ala Arg
                2005                2010                2015

gaa gcc aat gac aca gca aaa gct gtc ctg gcc cag gtt aag gac ctg   6096
Glu Ala Asn Asp Thr Ala Lys Ala Val Leu Ala Gln Val Lys Asp Leu
            2020                2025                2030

cat cag aac cta gat ggc ctg aag caa aac tac aat aaa ctg gca gac   6144
His Gln Asn Leu Asp Gly Leu Lys Gln Asn Tyr Asn Lys Leu Ala Asp
        2035                2040                2045

agc gtg gcc aaa acg aac gct gtg gtg aaa gat cct tcc aaa aac aaa   6192
Ser Val Ala Lys Thr Asn Ala Val Val Lys Asp Pro Ser Lys Asn Lys
    2050                2055                2060

atc att gca gat gca ggc act tcc gtg aga aat cta gaa cag gaa gct   6240
Ile Ile Ala Asp Ala Gly Thr Ser Val Arg Asn Leu Glu Gln Glu Ala
2065                2070                2075                2080

gac cgg cta atc gac aaa ctc aag ccc atc aag gag ctt gag gac aac   6288
Asp Arg Leu Ile Asp Lys Leu Lys Pro Ile Lys Glu Leu Glu Asp Asn
                2085                2090                2095

cta aag aaa aac att tct gaa ata aag gaa ctg atc aac caa gct cgg   6336
Leu Lys Lys Asn Ile Ser Glu Ile Lys Glu Leu Ile Asn Gln Ala Arg
            2100                2105                2110

aaa caa gct aac tct atc aaa gta tct gtt tct tcg gga ggt gac tgt   6384
Lys Gln Ala Asn Ser Ile Lys Val Ser Val Ser Ser Gly Gly Asp Cys
        2115                2120                2125

gtt cgg aca tac agg cca gaa atc aag aaa gga agc tac aat aac atc   6432
Val Arg Thr Tyr Arg Pro Glu Ile Lys Lys Gly Ser Tyr Asn Asn Ile
    2130                2135                2140

gtt gtc cat gtc aag acc gct gtt gcc gac aac ctc ctt ttt tat ctt   6480
Val Val His Val Lys Thr Ala Val Ala Asp Asn Leu Leu Phe Tyr Leu
2145                2150                2155                2160
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gga agt gcc aaa ttt att gac ttt ctt gct ata gaa atg cgc aaa ggc   6528
Gly Ser Ala Lys Phe Ile Asp Phe Leu Ala Ile Glu Met Arg Lys Gly
              2165                2170                2175

aaa gtc agc ttc ctc tgg att gtt ggc tct gga gtt ggc cga gta ggg   6576
Lys Val Ser Phe Leu Trp Ile Val Gly Ser Gly Val Gly Arg Val Gly
          2180                2185                2190

ttt cca gac ttg acc atc gac gac tcc tat tgg tac cgt att gaa gca   6624
Phe Pro Asp Leu Thr Ile Asp Asp Ser Tyr Trp Tyr Arg Ile Glu Ala
      2195                2200                2205

tca aga acg gga aga aat gga tct att tct gtg aga gct tta gat gga   6672
Ser Arg Thr Gly Arg Asn Gly Ser Ile Ser Val Arg Ala Leu Asp Gly
  2210                2215                2220

ccc aaa gcc agt atg gta ccc agc acc tac cat tca gtg tct cct ccc   6720
Pro Lys Ala Ser Met Val Pro Ser Thr Tyr His Ser Val Ser Pro Pro
2225                2230                2235                2240

ggg tat act atc cta gat gtg gat gca aat gca atg ctg ttt gtt ggt   6768
Gly Tyr Thr Ile Leu Asp Val Asp Ala Asn Ala Met Leu Phe Val Gly
              2245                2250                2255

ggc ctg acc gga aaa ata aag aag gcc gat gct gta cgt gtg atc acc   6816
Gly Leu Thr Gly Lys Ile Lys Lys Ala Asp Ala Val Arg Val Ile Thr
          2260                2265                2270

ttc acc ggc tgt atg gga gaa aca tac ttt gac aac aaa cct ata ggt   6864
Phe Thr Gly Cys Met Gly Glu Thr Tyr Phe Asp Asn Lys Pro Ile Gly
      2275                2280                2285

tta tgg aac ttc cgg gag aaa gaa ggc gac tgt aag gga tgt act gtc   6912
Leu Trp Asn Phe Arg Glu Lys Glu Gly Asp Cys Lys Gly Cys Thr Val
  2290                2295                2300

agc cca caa gtg gaa gat agt gag ggg act att cag ttt gat ggt gaa   6960
Ser Pro Gln Val Glu Asp Ser Glu Gly Thr Ile Gln Phe Asp Gly Glu
2305                2310                2315                2320

ggc tat gca tta gtg agc cgg ccc atc cgc tgg tac ccc aac atc tcc   7008
Gly Tyr Ala Leu Val Ser Arg Pro Ile Arg Trp Tyr Pro Asn Ile Ser
              2325                2330                2335

aca gtc atg ttc aag ttc cgg aca ttt tca tca agt gct ctc ctg atg   7056
Thr Val Met Phe Lys Phe Arg Thr Phe Ser Ser Ser Ala Leu Leu Met
          2340                2345                2350

tat ctt gcc aca cga gac ctg aaa gat ttc atg agt gta gag ctc agt   7104
Tyr Leu Ala Thr Arg Asp Leu Lys Asp Phe Met Ser Val Glu Leu Ser
      2355                2360                2365

gat gga cat gtg aaa gtc agc tat gac ctg ggc tca gga atg act tcc   7152
Asp Gly His Val Lys Val Ser Tyr Asp Leu Gly Ser Gly Met Thr Ser
  2370                2375                2380

gtt gtc agc aat caa aac cat aat gat ggg aaa tgg aaa gca ttc acg   7200
Val Val Ser Asn Gln Asn His Asn Asp Gly Lys Trp Lys Ala Phe Thr
2385                2390                2395                2400

ctg tcg cgg att cag aaa caa gcc aac ata tcg att gtc gac atc gat   7248
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Leu Ser Arg Ile Gln Lys Gln Ala Asn Ile Ser Ile Val Asp Ile Asp
                2405                2410                2415

tct aac cag gag gag aat gta gct act tca tct tct gga aac aac ttt   7296
Ser Asn Gln Glu Glu Asn Val Ala Thr Ser Ser Ser Gly Asn Asn Phe
            2420                2425                2430

ggt ctt gac ttg aaa gca gat gac aaa ata tat ttt ggt ggc ctg cca   7344
Gly Leu Asp Leu Lys Ala Asp Asp Lys Ile Tyr Phe Gly Gly Leu Pro
        2435                2440                2445

act ctg aga aac ttg agt atg aaa gca agg cca gaa gtc aat gtg aag   7392
Thr Leu Arg Asn Leu Ser Met Lys Ala Arg Pro Glu Val Asn Val Lys
    2450                2455                2460

aaa tac tcc ggc tgc ctc aaa gat att gaa att tca aga aca cct tac   7440
Lys Tyr Ser Gly Cys Leu Lys Asp Ile Glu Ile Ser Arg Thr Pro Tyr
2465                2470                2475                2480

aat ata ctc agc agc cct gat tat gtt ggt gtg acc aaa ggc tgt tca   7488
Asn Ile Leu Ser Ser Pro Asp Tyr Val Gly Val Thr Lys Gly Cys Ser
                2485                2490                2495

ctg gag aat gtt aat aca gtt agt ttc ccc aag cct ggt ttt gtg gag   7536
Leu Glu Asn Val Asn Thr Val Ser Phe Pro Lys Pro Gly Phe Val Glu
            2500                2505                2510

ctt gcc gct gtg tct att gat gtt gga aca gaa atc aat ctg tcc ttt   7584
Leu Ala Ala Val Ser Ile Asp Val Gly Thr Glu Ile Asn Leu Ser Phe
        2515                2520                2525

agt acc agg aac gag tct ggg atc att ctc ttg gga agt gga ggg aca   7632
Ser Thr Arg Asn Glu Ser Gly Ile Ile Leu Leu Gly Ser Gly Gly Thr
    2530                2535                2540

ctc aca cca ccc agg aga aaa cgg aga caa acc aca cag gct tat tat   7680
Leu Thr Pro Pro Arg Arg Lys Arg Arg Gln Thr Thr Gln Ala Tyr Tyr
2545                2550                2555                2560

gcc ata ttc ctc aac aag ggc cgc ttg gaa gtg cat ctc tcc tcg ggg   7728
Ala Ile Phe Leu Asn Lys Gly Arg Leu Glu Val His Leu Ser Ser Gly
                2565                2570                2575

aca cgg aca atg agg aaa att gtc atc aaa ccg gag cca aat ttg ttt   7776
Thr Arg Thr Met Arg Lys Ile Val Ile Lys Pro Glu Pro Asn Leu Phe
            2580                2585                2590

cat gat ggg aga gaa cat tct gtc cac gta gaa aga acc aga ggc atc   7824
His Asp Gly Arg Glu His Ser Val His Val Glu Arg Thr Arg Gly Ile
        2595                2600                2605

ttc act gtt caa att gat gaa gac aga aga cat atc caa aac ctg aca   7872
Phe Thr Val Gln Ile Asp Glu Asp Arg Arg His Ile Gln Asn Leu Thr
    2610                2615                2620

gag gaa cag ccc atc gaa gtg aaa aag ctc ttt gtc ggg ggt gct cct   7920
Glu Glu Gln Pro Ile Glu Val Lys Lys Leu Phe Val Gly Gly Ala Pro
2625                2630                2635                2640

cct gaa ttt cag ccc tcc cca ctc agg aat att ccg gcc ttt caa ggc   7968
Pro Glu Phe Gln Pro Ser Pro Leu Arg Asn Ile Pro Ala Phe Gln Gly
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                2645                2650                2655

tgt gtg tgg aac ctt gtt att aac tcc atc ccc atg gac ttt gcg cag   8016
Cys Val Trp Asn Leu Val Ile Asn Ser Ile Pro Met Asp Phe Ala Gln
            2660                2665                2670

cct ata gcc ttc aaa aat gcc gac att ggt cgc tgt acc tat caa aag   8064
Pro Ile Ala Phe Lys Asn Ala Asp Ile Gly Arg Cys Thr Tyr Gln Lys
        2675                2680                2685

ccc cgg gaa gat gag agt gaa gca gtt cca gct gaa gtt att gtc cag   8112
Pro Arg Glu Asp Glu Ser Glu Ala Val Pro Ala Glu Val Ile Val Gln
    2690                2695                2700

cct cag tcg gtg ccc acc cct gcc ttc cct ttc cca gtc ccc acc atg   8160
Pro Gln Ser Val Pro Thr Pro Ala Phe Pro Phe Pro Val Pro Thr Met
2705                2710                2715                2720

gtg cat ggc cct tgt gtt gca gaa tca gaa cca gct ctt ctg aca ggg   8208
Val His Gly Pro Cys Val Ala Glu Ser Glu Pro Ala Leu Leu Thr Gly
                2725                2730                2735

agc aag cag ttt ggg ctt tcc aga aac agc cac att gca att gtc ttt   8256
Ser Lys Gln Phe Gly Leu Ser Arg Asn Ser His Ile Ala Ile Val Phe
            2740                2745                2750

gat gac acc aaa gtt aaa aac cgc ctc acc att gag ctg gag gta cga   8304
Asp Asp Thr Lys Val Lys Asn Arg Leu Thr Ile Glu Leu Glu Val Arg
        2755                2760                2765

act gaa gct gaa tca ggc ttg ctc ttc tac atg ggt cgg atc aat cat   8352
Thr Glu Ala Glu Ser Gly Leu Leu Phe Tyr Met Gly Arg Ile Asn His
    2770                2775                2780

gct gat ttt ggt act gtt cag ctg agg aat ggg ttc ccg ttc ttc agt   8400
Ala Asp Phe Gly Thr Val Gln Leu Arg Asn Gly Phe Pro Phe Phe Ser
2785                2790                2795                2800

tat gat ttg ggg agt ggg agc acc aga acc atg atc ccc aca aaa atc   8448
Tyr Asp Leu Gly Ser Gly Ser Thr Arg Thr Met Ile Pro Thr Lys Ile
                2805                2810                2815

aac gat ggt cag tgg cac aag att aag att gtg aga gtg aag cag gag   8496
Asn Asp Gly Gln Trp His Lys Ile Lys Ile Val Arg Val Lys Gln Glu
            2820                2825                2830

gga att ctt tat gtg gat gat gcc tcc agc caa acc atc agt ccc aag   8544
Gly Ile Leu Tyr Val Asp Asp Ala Ser Ser Gln Thr Ile Ser Pro Lys
        2835                2840                2845

aaa gcc gac atc ctg gat gtc ggg ggg att ctg tat gtc ggt gga ttg   8592
Lys Ala Asp Ile Leu Asp Val Gly Gly Ile Leu Tyr Val Gly Gly Leu
    2850                2855                2860

ccg atc aac tat acc aca cgc aga att ggt cca gtg act tac agc ctg   8640
Pro Ile Asn Tyr Thr Thr Arg Arg Ile Gly Pro Val Thr Tyr Ser Leu
2865                2870                2875                2880

gat ggc tgt gtt agg aat ctt cac atg gaa caa gcc cct gtt gat ctg   8688
Asp Gly Cys Val Arg Asn Leu His Met Glu Gln Ala Pro Val Asp Leu
                2885                2890                2895
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gac cag cct acc tcc agc ttt cac gtt ggg aca tgc ttt gcg aat gca   8736
Asp Gln Pro Thr Ser Ser Phe His Val Gly Thr Cys Phe Ala Asn Ala
          2900                2905                2910

gag agt ggg act tac ttt gat gga acc ggt ttt ggt aaa gca gtt ggt   8784
Glu Ser Gly Thr Tyr Phe Asp Gly Thr Gly Phe Gly Lys Ala Val Gly
       2915                2920                2925

ggg ttc atc gtt gga ttg gac ctt ctt gtg gaa ttt gaa ttc cgt acc   8832
Gly Phe Ile Val Gly Leu Asp Leu Leu Val Glu Phe Glu Phe Arg Thr
   2930                2935                2940

aca aga ccc act ggg gtc ctc ctg ggg atc agc agt cag aag atg gat   8880
Thr Arg Pro Thr Gly Val Leu Leu Gly Ile Ser Ser Gln Lys Met Asp
2945                2950                2955                2960

gga atg ggt att gaa atg atc gac gag aag ctt atg ttc cac gtg gat   8928
Gly Met Gly Ile Glu Met Ile Asp Glu Lys Leu Met Phe His Val Asp
              2965                2970                2975

aat ggc gct ggc cga ttc act gca att tat gat gct gag atc cca ggc   8976
Asn Gly Ala Gly Arg Phe Thr Ala Ile Tyr Asp Ala Glu Ile Pro Gly
          2980                2985                2990

cac atg tgc aat gga cag tgg tat aaa gtc act gcc aag aag atc aaa   9024
His Met Cys Asn Gly Gln Trp Tyr Lys Val Thr Ala Lys Lys Ile Lys
       2995                3000                3005

aac cgt ctt gag ctg gtg gta gat ggg aac cag gtg gat gcc cag agc   9072
Asn Arg Leu Glu Leu Val Val Asp Gly Asn Gln Val Asp Ala Gln Ser
   3010                3015                3020

cca aac tca gca tcg aca tca gct gat aca aac gac cct gtt ttc gtt   9120
Pro Asn Ser Ala Ser Thr Ser Ala Asp Thr Asn Asp Pro Val Phe Val
3025                3030                3035                3040

ggc ggt ttc cca ggt ggc ctc aat cag ttt ggc ctg acc acc aac att   9168
Gly Gly Phe Pro Gly Gly Leu Asn Gln Phe Gly Leu Thr Thr Asn Ile
              3045                3050                3055

agg ttc cga ggc tgc atc cga tct ctg aag ctc acc aaa ggc act gca   9216
Arg Phe Arg Gly Cys Ile Arg Ser Leu Lys Leu Thr Lys Gly Thr Ala
          3060                3065                3070

aac cgc tgg agg tta att ttg cca agg ccc tgg aac tgaggggtgt        9262
Asn Arg Trp Arg Leu Ile Leu Pro Arg Pro Trp Asn
       3075                3080

tcaacctgta tcatgcccga ctacctaata aagatagttc aatcctgagg agaattcatc 9322

aaaacaagta tatcaagtta aacaatatac actcctatca tattaataaa actaatgtgc 9382

agcggccgc                                                        9391


<210> 12
<211> 3084
<212> PRT
<213> Mus musculus
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<400> 12

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Gln Arg Arg Gln Ser Gln Ala His Gln Gln Arg Gly Leu Phe Pro Ala
 1               5                  10                  15

Val Leu Asn Leu Ala Ser Asn Ala Leu Ile Thr Thr Asn Ala Thr Cys
            20                  25                  30

Gly Glu Lys Gly Pro Glu Met Tyr Cys Lys Leu Val Glu His Val Pro
        35                  40                  45

Gly Gln Pro Val Arg Asn Pro Gln Cys Arg Ile Cys Asn Gln Asn Ser
    50                  55                  60

Ser Asn Pro Tyr Gln Arg His Pro Ile Thr Asn Ala Ile Asp Gly Lys
65                  70                  75                  80

Asn Thr Trp Trp Gln Ser Pro Ser Ile Lys Asn Gly Val Glu Tyr His
                85                  90                  95

Tyr Val Thr Ile Thr Leu Asp Leu Gln Gln Val Phe Gln Ile Ala Tyr
            100                 105                 110

Val Ile Val Lys Ala Ala Asn Ser Pro Arg Pro Gly Asn Trp Ile Leu
        115                 120                 125

Glu Arg Ser Leu Asp Asp Val Glu Tyr Lys Pro Trp Gln Tyr His Ala
    130                 135                 140

Val Thr Asp Thr Glu Cys Leu Thr Leu Tyr Asn Ile Tyr Pro Arg Thr
145                 150                 155                 160

Gly Pro Pro Ser Tyr Ala Lys Asp Asp Glu Val Ile Cys Thr Ser Phe
                165                 170                 175

Tyr Ser Lys Ile His Pro Leu Glu Asn Gly Glu Ile His Ile Ser Leu
            180                 185                 190

Ile Asn Gly Arg Pro Ser Ala Asp Asp Pro Ser Pro Glu Leu Leu Glu
        195                 200                 205

Phe Thr Ser Ala Arg Tyr Ile Arg Leu Arg Phe Gln Arg Ile Arg Thr
    210                 215                 220

Leu Asn Ala Asp Leu Met Met Phe Ala His Lys Asp Pro Arg Glu Ile
225                 230                 235                 240

Asp Pro Ile Val Thr Arg Arg Tyr Tyr Tyr Ser Val Lys Asp Ile Ser
                245                 250                 255

Val Gly Gly Met Cys Ile Cys Tyr Gly His Ala Arg Ala Cys Pro Leu
            260                 265                 270

Asp Pro Ala Thr Asn Lys Ser Arg Cys Glu Cys Glu His Asn Thr Cys
        275                 280                 285

Gly Glu Ser Cys Asp Arg Cys Cys Pro Gly Phe His Gln Lys Pro Trp
    290                 295                 300

Arg Ala Gly Thr Phe Leu Thr Lys Ser Glu Cys Glu Ala Cys Asn Cys
305                 310                 315                 320
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His Gly Lys Ala Glu Glu Cys Tyr Tyr Asp Glu Thr Val Ala Ser Arg
                325                 330                 335

Asn Leu Ser Leu Asn Ile His Gly Lys Tyr Ile Gly Gly Gly Val Cys
            340                 345                 350

Ile Asn Cys Thr His Asn Thr Ala Gly Ile Asn Cys Glu Thr Cys Val
        355                 360                 365

Asp Gly Phe Phe Arg Pro Lys Gly Val Ser Pro Asn Tyr Pro Arg Pro
    370                 375                 380

Cys Gln Pro Cys His Cys Asp Pro Thr Gly Ser Leu Ser Glu Val Cys
385                 390                 395                 400

Val Lys Asp Glu Lys Tyr Ala Gln Arg Gly Leu Lys Pro Gly Ser Cys
                405                 410                 415

His Cys Lys Thr Gly Phe Gly Gly Val Asn Cys Asp Arg Cys Val Arg
            420                 425                 430

Gly Tyr His Gly Tyr Pro Asp Cys Gln Pro Cys Asn Cys Ser Gly Leu
        435                 440                 445

Gly Ser Thr Asn Glu Asp Pro Cys Val Gly Pro Cys Ser Cys Lys Glu
    450                 455                 460

Asn Val Glu Gly Glu Asp Cys Ser Arg Cys Lys Ser Gly Phe Phe Asn
465                 470                 475                 480

Leu Gln Glu Asp Asn Gln Lys Gly Cys Glu Glu Cys Phe Cys Ser Gly
                485                 490                 495

Val Ser Asn Arg Cys Gln Ser Ser Tyr Trp Thr Tyr Gly Asn Ile Gln
            500                 505                 510

Asp Met Arg Gly Trp Tyr Leu Thr Asp Leu Ser Gly Arg Ile Arg Met
        515                 520                 525

Ala Pro Gln Leu Asp Asn Pro Asp Ser Pro Gln Gln Ile Ser Ile Ser
    530                 535                 540

Asn Ser Glu Ala Arg Lys Ser Leu Leu Asp Gly Tyr Tyr Trp Ser Ala
545                 550                 555                 560

Pro Pro Pro Tyr Leu Gly Asn Arg Leu Pro Ala Val Gly Gly Gln Leu
                565                 570                 575

Ser Phe Thr Ile Ser Tyr Asp Leu Glu Glu Glu Glu Asp Asp Thr Glu
            580                 585                 590

Lys Leu Leu Gln Leu Met Ile Ile Phe Glu Gly Asn Asp Leu Arg Ile
        595                 600                 605

Ser Thr Ala Tyr Lys Glu Val Tyr Leu Glu Pro Ser Glu Glu His Val
    610                 615                 620

Glu Glu Val Ser Leu Lys Glu Glu Ala Phe Thr Ile His Gly Thr Asn
625                 630                 635                 640

Leu Pro Val Thr Arg Lys Asp Phe Met Ile Val Leu Thr Asn Leu Gly
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                645                 650                 655

Glu Ile Leu Ile Gln Ile Thr Tyr Asn Leu Gly Met Asp Ala Ile Phe
            660                 665                 670

Arg Leu Ser Ser Val Asn Leu Glu Ser Pro Val Pro Tyr Pro Thr Asp
        675                 680                 685

Arg Arg Ile Ala Thr Asp Val Glu Val Cys Gln Cys Pro Pro Gly Tyr
    690                 695                 700

Ser Gly Ser Ser Cys Glu Thr Cys Trp Pro Arg His Arg Arg Val Asn
705                 710                 715                 720

Gly Thr Ile Phe Gly Gly Ile Cys Glu Pro Cys Gln Cys Phe Ala His
                725                 730                 735

Ala Glu Ala Cys Asp Asp Ile Thr Gly Glu Cys Leu Asn Cys Lys Asp
            740                 745                 750

His Thr Gly Gly Pro Tyr Cys Asn Glu Cys Leu Pro Gly Phe Tyr Gly
        755                 760                 765

Asp Pro Thr Arg Gly Ser Pro Glu Asp Cys Gln Pro Cys Ala Cys Pro
    770                 775                 780

Leu Asn Ile Pro Ser Asn Asn Phe Ser Pro Thr Cys His Leu Asp Arg
785                 790                 795                 800

Ser Leu Gly Leu Ile Cys Asp Glu Cys Pro Ile Gly Tyr Thr Gly Pro
                805                 810                 815

Arg Cys Glu Arg Cys Ala Glu Gly Tyr Phe Gly Gln Pro Ser Val Pro
            820                 825                 830

Gly Gly Ser Cys Gln Pro Cys Gln Cys Asn Asp Asn Leu Asp Tyr Ser
        835                 840                 845

Ile Pro Gly Ser Cys Asp Ser Leu Ser Gly Ser Cys Leu Ile Cys Lys
    850                 855                 860

Pro Gly Thr Thr Gly Arg Tyr Cys Glu Leu Cys Ala Asp Gly Tyr Phe
865                 870                 875                 880

Gly Asp Ala Val Asn Thr Lys Asn Cys Gln Pro Cys Arg Cys Asp Ile
                885                 890                 895

Asn Gly Ser Phe Ser Glu Asp Cys His Thr Arg Thr Gly Gln Cys Glu
            900                 905                 910

Cys Arg Pro Asn Val Gln Gly Arg His Cys Asp Glu Cys Lys Pro Glu
        915                 920                 925

Thr Phe Gly Leu Gln Leu Gly Arg Gly Cys Leu Pro Cys Asn Cys Asn
    930                 935                 940

Ser Phe Gly Ser Lys Ser Phe Asp Cys Glu Ala Ser Gly Gln Cys Trp
945                 950                 955                 960

Cys Gln Pro Gly Val Ala Gly Lys Lys Cys Asp Arg Cys Ala His Gly
                965                 970                 975
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Tyr Phe Asn Phe Gln Glu Gly Gly Cys Ile Ala Cys Asp Cys Ser His
            980                 985                 990

Leu Gly Asn Asn Cys Asp Pro Lys Thr Gly Gln Cys Ile Cys Pro Pro
        995                1000                1005

Asn Thr Thr Gly Glu Lys Cys Ser Glu Cys Leu Pro Asn Thr Trp Gly
   1010                1015                1020

His Ser Ile Val Thr Gly Cys Lys Val Cys Asn Cys Ser Thr Val Gly
1025               1030                1035                1040

Ser Leu Ala Ser Gln Cys Asn Val Asn Thr Gly Gln Cys Ser Cys His
                1045                1050                1055

Pro Lys Phe Ser Gly Met Lys Cys Ser Glu Cys Ser Arg Gly His Trp
           1060                1065                1070

Asn Tyr Pro Leu Cys Thr Leu Cys Asp Cys Phe Leu Pro Gly Thr Asp
       1075                1080                1085

Ala Thr Thr Cys Asp Leu Glu Thr Arg Lys Cys Ser Cys Ser Asp Gln
   1090                1095                1100

Thr Gly Gln Cys Ser Cys Lys Val Asn Val Glu Gly Val His Cys Asp
1105               1110                1115                1120

Arg Cys Arg Pro Gly Lys Phe Gly Leu Asp Ala Lys Asn Pro Leu Gly
                1125                1130                1135

Cys Ser Ser Cys Tyr Cys Phe Gly Val Thr Ser Gln Cys Ser Glu Ala
           1140                1145                1150

Lys Gly Leu Ile Arg Thr Trp Val Thr Leu Ser Asp Glu Gln Thr Ile
       1155                1160                1165

Leu Pro Leu Val Asp Glu Ala Leu Gln His Thr Thr Thr Lys Gly Ile
   1170                1175                1180

Ala Phe Gln Lys Pro Glu Ile Val Ala Lys Met Asp Glu Val Arg Gln
1185               1190                1195                1200

Glu Leu His Leu Glu Pro Phe Tyr Trp Lys Leu Pro Gln Gln Phe Glu
                1205                1210                1215

Gly Lys Lys Leu Met Ala Tyr Gly Gly Lys Leu Lys Tyr Ala Ile Tyr
           1220                1225                1230

Phe Glu Ala Arg Asp Glu Thr Gly Phe Ala Thr Tyr Lys Pro Gln Val
       1235                1240                1245

Ile Ile Arg Gly Gly Thr Pro Thr His Ala Arg Ile Ile Thr Arg His
   1250                1255                1260

Met Ala Ala Pro Leu Ile Gly Gln Leu Thr Arg His Glu Ile Glu Met
1265               1270                1275                1280

Thr Glu Lys Glu Trp Lys Tyr Tyr Gly Asp Asp Pro Arg Ile Ser Arg
                1285                1290                1295
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Thr Val Thr Arg Glu Asp Phe Leu Asp Ile Leu Tyr Asp Ile His Tyr
          1300                1305                1310

Ile Leu Ile Lys Ala Thr Tyr Gly Asn Val Val Arg Gln Ser Arg Ile
       1315                1320                1325

Ser Glu Ile Ser Met Glu Val Ala Glu Pro Gly His Val Leu Ala Gly
   1330                1335                1340

Ser Pro Pro Ala His Leu Ile Glu Arg Cys Asp Cys Pro Pro Gly Tyr
1345                1350                1355                1360

Ser Gly Leu Ser Cys Glu Thr Cys Ala Pro Gly Phe Tyr Arg Leu Arg
               1365                1370                1375

Ser Glu Pro Gly Gly Arg Thr Pro Gly Pro Thr Leu Gly Thr Cys Val
          1380                1385                1390

Pro Cys Gln Cys Asn Gly His Ser Ser Gln Cys Asp Pro Glu Thr Ser
       1395                1400                1405

Val Cys Gln Asn Cys Gln His His Thr Ala Gly Asp Phe Cys Glu Arg
   1410                1415                1420

Cys Ala Leu Gly Tyr Tyr Gly Ile Val Arg Gly Leu Pro Asn Asp Cys
1425                1430                1435                1440

Gln Pro Cys Ala Cys Pro Leu Ile Ser Pro Ser Asn Asn Phe Ser Pro
               1445                1450                1455

Ser Cys Val Leu Glu Gly Leu Glu Asp Tyr Arg Cys Thr Ala Cys Pro
          1460                1465                1470

Arg Gly Tyr Glu Gly Gln Tyr Cys Glu Arg Cys Ala Pro Gly Tyr Thr
       1475                1480                1485

Gly Ser Pro Ser Ser Pro Gly Gly Ser Cys Gln Glu Cys Glu Cys Asp
   1490                1495                1500

Pro Tyr Gly Ser Leu Pro Val Pro Cys Asp Arg Val Thr Gly Leu Cys
1505                1510                1515                1520

Thr Cys Arg Pro Gly Ala Thr Gly Arg Lys Cys Asp Gly Cys Glu His
               1525                1530                1535

Trp His Ala Arg Glu Gly Ala Glu Cys Val Phe Cys Gly Asp Glu Cys
          1540                1545                1550

Thr Gly Leu Leu Leu Gly Asp Leu Ala Arg Leu Glu Gln Met Thr Met
       1555                1560                1565

Asn Ile Asn Leu Thr Gly Pro Leu Pro Ala Pro Tyr Lys Ile Leu Tyr
   1570                1575                1580

Gly Leu Glu Asn Thr Thr Gln Glu Leu Lys His Leu Leu Ser Pro Gln
1585                1590                1595                1600

Arg Ala Pro Glu Arg Leu Ile Gln Leu Ala Glu Gly Asn Val Asn Thr
               1605                1610                1615

Leu Val Met Glu Thr Asn Glu Leu Leu Thr Arg Ala Thr Lys Val Thr
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          1620                1625                1630

Ala Asp Gly Glu Gln Thr Gly Gln Asp Ala Glu Arg Thr Asn Ser Arg
       1635                1640                1645

Ala Glu Ser Leu Glu Glu Phe Ile Lys Gly Leu Val Gln Asp Ala Glu
   1650                1655                1660

Ala Ile Asn Glu Lys Ala Val Lys Leu Asn Glu Thr Leu Gly Asn Gln
1665                1670                1675                1680

Asp Lys Thr Ala Glu Arg Asn Leu Glu Glu Leu Gln Lys Glu Ile Asp
               1685                1690                1695

Arg Met Leu Lys Glu Leu Arg Ser Lys Asp Leu Gln Thr Gln Lys Glu
           1700                1705                1710

Val Ala Glu Asp Glu Leu Val Ala Ala Glu Gly Leu Leu Lys Arg Val
       1715                1720                1725

Asn Lys Leu Phe Gly Glu Pro Arg Ala Gln Asn Glu Asp Met Glu Lys
   1730                1735                1740

Asp Leu Gln Gln Lys Leu Ala Glu Tyr Lys Asn Lys Leu Asp Asp Ala
1745                1750                1755                1760

Trp Asp Leu Leu Arg Glu Ala Thr Asp Lys Thr Arg Asp Ala Asn Arg
               1765                1770                1775

Leu Ser Ala Ala Asn Gln Lys Asn Met Thr Ile Leu Glu Thr Lys Lys
           1780                1785                1790

Glu Ala Ile Glu Gly Ser Lys Arg Gln Ile Glu Asn Thr Leu Lys Glu
       1795                1800                1805

Gly Asn Asp Ile Leu Asp Glu Ala Asn Gln Leu Leu Gly Glu Ile Asn
   1810                1815                1820

Ser Val Ile Asp Tyr Val Asp Asp Ile Lys Thr Lys Leu Pro Pro Met
1825                1830                1835                1840

Ser Glu Glu Leu Ser Asp Lys Ile Asp Asp Leu Ala Gln Glu Ile Lys
               1845                1850                1855

Asp Arg Arg Leu Ala Glu Lys Val Phe Gln Ala Glu Ser His Ala Ala
           1860                1865                1870

Gln Leu Asn Asp Ser Ser Ala Val Leu Asp Gly Ile Leu Asp Glu Ala
       1875                1880                1885

Lys Asn Ile Ser Phe Asn Ala Thr Ala Ala Phe Arg Ala Tyr Ser Asn
   1890                1895                1900

Ile Lys Asp Tyr Ile Asp Glu Ala Glu Lys Val Ala Arg Glu Ala Lys
1905                1910                1915                1920

Glu Leu Ala Gln Gly Ala Thr Lys Leu Ala Thr Ser Pro Gln Gly Leu
               1925                1930                1935

Leu Lys Glu Asp Ala Lys Gly Ser Leu Gln Lys Ser Phe Arg Ile Leu
           1940                1945                1950
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Asn Glu Ala Lys Lys Leu Ala Asn Asp Val Lys Gly Asn His Asn Asp
       1955                1960                1965

Leu Asn Asp Leu Lys Thr Arg Leu Glu Thr Ala Asp Leu Arg Asn Ser
   1970                1975                1980

Gly Leu Leu Gly Ala Leu Asn Asp Thr Met Asp Lys Leu Ser Ala Ile
1985                1990                1995                2000

Thr Asn Asp Thr Ala Ala Lys Leu Gln Ala Val Lys Glu Lys Ala Arg
                2005                2010                2015

Glu Ala Asn Asp Thr Ala Lys Ala Val Leu Ala Gln Val Lys Asp Leu
           2020                2025                2030

His Gln Asn Leu Asp Gly Leu Lys Gln Asn Tyr Asn Lys Leu Ala Asp
       2035                2040                2045

Ser Val Ala Lys Thr Asn Ala Val Val Lys Asp Pro Ser Lys Asn Lys
   2050                2055                2060

Ile Ile Ala Asp Ala Gly Thr Ser Val Arg Asn Leu Glu Gln Glu Ala
2065                2070                2075                2080

Asp Arg Leu Ile Asp Lys Leu Lys Pro Ile Lys Glu Leu Glu Asp Asn
                2085                2090                2095

Leu Lys Lys Asn Ile Ser Glu Ile Lys Glu Leu Ile Asn Gln Ala Arg
           2100                2105                2110

Lys Gln Ala Asn Ser Ile Lys Val Ser Val Ser Ser Gly Gly Asp Cys
       2115                2120                2125

Val Arg Thr Tyr Arg Pro Glu Ile Lys Lys Gly Ser Tyr Asn Asn Ile
   2130                2135                2140

Val Val His Val Lys Thr Ala Val Ala Asp Asn Leu Leu Phe Tyr Leu
2145                2150                2155                2160

Gly Ser Ala Lys Phe Ile Asp Phe Leu Ala Ile Glu Met Arg Lys Gly
                2165                2170                2175

Lys Val Ser Phe Leu Trp Ile Val Gly Ser Gly Val Gly Arg Val Gly
           2180                2185                2190

Phe Pro Asp Leu Thr Ile Asp Asp Ser Tyr Trp Tyr Arg Ile Glu Ala
       2195                2200                2205

Ser Arg Thr Gly Arg Asn Gly Ser Ile Ser Val Arg Ala Leu Asp Gly
   2210                2215                2220

Pro Lys Ala Ser Met Val Pro Ser Thr Tyr His Ser Val Ser Pro Pro
2225                2230                2235                2240

Gly Tyr Thr Ile Leu Asp Val Asp Ala Asn Ala Met Leu Phe Val Gly
                2245                2250                2255

Gly Leu Thr Gly Lys Ile Lys Lys Ala Asp Ala Val Arg Val Ile Thr
           2260                2265                2270
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Phe Thr Gly Cys Met Gly Glu Thr Tyr Phe Asp Asn Lys Pro Ile Gly
      2275                2280                2285

Leu Trp Asn Phe Arg Glu Lys Glu Gly Asp Cys Lys Gly Cys Thr Val
   2290                2295                2300

Ser Pro Gln Val Glu Asp Ser Glu Gly Thr Ile Gln Phe Asp Gly Glu
2305                2310                2315                2320

Gly Tyr Ala Leu Val Ser Arg Pro Ile Arg Trp Tyr Pro Asn Ile Ser
                2325                2330                2335

Thr Val Met Phe Lys Phe Arg Thr Phe Ser Ser Ser Ala Leu Leu Met
           2340                2345                2350

Tyr Leu Ala Thr Arg Asp Leu Lys Asp Phe Met Ser Val Glu Leu Ser
      2355                2360                2365

Asp Gly His Val Lys Val Ser Tyr Asp Leu Gly Ser Gly Met Thr Ser
   2370                2375                2380

Val Val Ser Asn Gln Asn His Asn Asp Gly Lys Trp Lys Ala Phe Thr
2385                2390                2395                2400

Leu Ser Arg Ile Gln Lys Gln Ala Asn Ile Ser Ile Val Asp Ile Asp
                2405                2410                2415

Ser Asn Gln Glu Glu Asn Val Ala Thr Ser Ser Ser Gly Asn Asn Phe
           2420                2425                2430

Gly Leu Asp Leu Lys Ala Asp Asp Lys Ile Tyr Phe Gly Gly Leu Pro
      2435                2440                2445

Thr Leu Arg Asn Leu Ser Met Lys Ala Arg Pro Glu Val Asn Val Lys
   2450                2455                2460

Lys Tyr Ser Gly Cys Leu Lys Asp Ile Glu Ile Ser Arg Thr Pro Tyr
2465                2470                2475                2480

Asn Ile Leu Ser Ser Pro Asp Tyr Val Gly Val Thr Lys Gly Cys Ser
                2485                2490                2495

Leu Glu Asn Val Asn Thr Val Ser Phe Pro Lys Pro Gly Phe Val Glu
           2500                2505                2510

Leu Ala Ala Val Ser Ile Asp Val Gly Thr Glu Ile Asn Leu Ser Phe
      2515                2520                2525

Ser Thr Arg Asn Glu Ser Gly Ile Ile Leu Leu Gly Ser Gly Gly Thr
   2530                2535                2540

Leu Thr Pro Pro Arg Arg Lys Arg Arg Gln Thr Thr Gln Ala Tyr Tyr
2545                2550                2555                2560

Ala Ile Phe Leu Asn Lys Gly Arg Leu Glu Val His Leu Ser Ser Gly
                2565                2570                2575

Thr Arg Thr Met Arg Lys Ile Val Ile Lys Pro Glu Pro Asn Leu Phe
           2580                2585                2590

His Asp Gly Arg Glu His Ser Val His Val Glu Arg Thr Arg Gly Ile
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      2595                2600                2605

Phe Thr Val Gln Ile Asp Glu Asp Arg Arg His Ile Gln Asn Leu Thr
   2610                2615                2620

Glu Glu Gln Pro Ile Glu Val Lys Lys Leu Phe Val Gly Gly Ala Pro
2625                2630                2635                2640

Pro Glu Phe Gln Pro Ser Pro Leu Arg Asn Ile Pro Ala Phe Gln Gly
               2645                2650                2655

Cys Val Trp Asn Leu Val Ile Asn Ser Ile Pro Met Asp Phe Ala Gln
          2660                2665                2670

Pro Ile Ala Phe Lys Asn Ala Asp Ile Gly Arg Cys Thr Tyr Gln Lys
       2675                2680                2685

Pro Arg Glu Asp Glu Ser Glu Ala Val Pro Ala Glu Val Ile Val Gln
   2690                2695                2700

Pro Gln Ser Val Pro Thr Pro Ala Phe Pro Phe Pro Val Pro Thr Met
2705                2710                2715                2720

Val His Gly Pro Cys Val Ala Glu Ser Glu Pro Ala Leu Leu Thr Gly
               2725                2730                2735

Ser Lys Gln Phe Gly Leu Ser Arg Asn Ser His Ile Ala Ile Val Phe
          2740                2745                2750

Asp Asp Thr Lys Val Lys Asn Arg Leu Thr Ile Glu Leu Glu Val Arg
       2755                2760                2765

Thr Glu Ala Glu Ser Gly Leu Leu Phe Tyr Met Gly Arg Ile Asn His
   2770                2775                2780

Ala Asp Phe Gly Thr Val Gln Leu Arg Asn Gly Phe Pro Phe Phe Ser
2785                2790                2795                2800

Tyr Asp Leu Gly Ser Gly Ser Thr Arg Thr Met Ile Pro Thr Lys Ile
               2805                2810                2815

Asn Asp Gly Gln Trp His Lys Ile Lys Ile Val Arg Val Lys Gln Glu
          2820                2825                2830

Gly Ile Leu Tyr Val Asp Asp Ala Ser Ser Gln Thr Ile Ser Pro Lys
       2835                2840                2845

Lys Ala Asp Ile Leu Asp Val Gly Gly Ile Leu Tyr Val Gly Gly Leu
   2850                2855                2860

Pro Ile Asn Tyr Thr Thr Arg Arg Ile Gly Pro Val Thr Tyr Ser Leu
2865                2870                2875                2880

Asp Gly Cys Val Arg Asn Leu His Met Glu Gln Ala Pro Val Asp Leu
               2885                2890                2895

Asp Gln Pro Thr Ser Ser Phe His Val Gly Thr Cys Phe Ala Asn Ala
          2900                2905                2910

Glu Ser Gly Thr Tyr Phe Asp Gly Thr Gly Phe Gly Lys Ala Val Gly
       2915                2920                2925
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Gly Phe Ile Val Gly Leu Asp Leu Leu Val Glu Phe Glu Phe Arg Thr
   2930                2935                2940

Thr Arg Pro Thr Gly Val Leu Leu Gly Ile Ser Ser Gln Lys Met Asp
2945                2950                2955                2960

Gly Met Gly Ile Glu Met Ile Asp Glu Lys Leu Met Phe His Val Asp
               2965                2970                2975

Asn Gly Ala Gly Arg Phe Thr Ala Ile Tyr Asp Ala Glu Ile Pro Gly
           2980                2985                2990

His Met Cys Asn Gly Gln Trp Tyr Lys Val Thr Ala Lys Lys Ile Lys
       2995                3000                3005

Asn Arg Leu Glu Leu Val Val Asp Gly Asn Gln Val Asp Ala Gln Ser
   3010                3015                3020

Pro Asn Ser Ala Ser Thr Ser Ala Asp Thr Asn Asp Pro Val Phe Val
3025                3030                3035                3040

Gly Gly Phe Pro Gly Gly Leu Asn Gln Phe Gly Leu Thr Thr Asn Ile
               3045                3050                3055

Arg Phe Arg Gly Cys Ile Arg Ser Leu Lys Leu Thr Lys Gly Thr Ala
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Asn Arg Trp Arg Leu Ile Leu Pro Arg Pro Trp Asn
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atg ggg ctt ctc cag ttg cta gct ttc agt ttc tta gcc ctg tgc aga   165
Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Ala Leu Cys Arg
  1               5                  10                  15

gcc cga gtg cgc gct cag gaa ccc gag ttc agc tac ggc tgc gca gaa   213
Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu
             20                  25                  30

ggc agc tgc tat ccc gcc acg ggc gac ctt ctc atc ggc cga gca cag   261
Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln
         35                  40                  45
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aag ctt tcg gtg acc tcg acg tgc ggg ctg cac aag ccc gaa ccc tac   309
Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
     50                  55                  60

tgt atc gtc agc cac ttg cag gag gac aaa aaa tgc ttc ata tgc aat   357
Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn
 65                  70                  75                  80

tcc caa gat cct tat cat gag acc ctg aat cct gac agc cat ctc att   405
Ser Gln Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile
                 85                  90                  95

gaa aat gtg gtc act aca ttt gct cca aac cgc ctt aag att tgg tgg   453
Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp
            100                 105                 110

caa tct gaa aat ggt gtg gaa aat gta act atc caa ctg gat ttg gaa   501
Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu
        115                 120                 125

gca gaa ttc cat ttt act cat ctc ata atg act ttc aag aca ttc cgt   549
Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg
    130                 135                 140

cca gct gct atg ctg ata gaa cga tcg tcc gac ttt ggg aaa acc tgg   597
Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp
145                 150                 155                 160

ggt gtg tat aga tac ttc gcc tat gac tgt gag gcc tcg ttt cca ggc   645
Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly
                165                 170                 175

att tca act ggc ccc atg aaa aaa gtc gat gac ata att tgt gat tct   693
Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser
            180                 185                 190

cga tat tct gac att gaa ccc tca act gaa gga gag gtg ata ttt cgt   741
Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg
        195                 200                 205

gct tta gat cct gct ttc aaa ata gaa gat cct tat agc cca agg ata   789
Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile
    210                 215                 220

cag aat tta tta aaa att acc aac ttg aga atc aag ttt gtg aaa ctg   837
Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu
225                 230                 235                 240

cat act ttg gga gat aac ctt ctg gat tcc agg atg gaa atc aga gaa   885
His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu
                245                 250                 255

aag tat tat tat gca gtt tat gat atg gtg gtt cga gga aat tgc ttc   933
Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe
            260                 265                 270

tgc tat ggt cat gcc agc gaa tgt gcc cct gtg gat gga ttc aat gaa   981
Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu
        275                 280                 285
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gaa gtg gaa gga atg gtt cac gga cac tgc atg tgc agg cat aac acc   1029
Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr
    290                 295                 300

aag ggc tta aac tgt gaa ctc tgc atg gat ttc tac cat gat tta cct   1077
Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro
305                 310                 315                 320

tgg aga cct gct gaa ggc cga aac agc aac gcc tgt aaa aaa tgt aac   1125
Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn
                325                 330                 335

tgc aat gaa cat tcc atc tct tgt cac ttt gac atg gct gtt tac ctg   1173
Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu
            340                 345                 350

gcc acg ggg aac gtc agc gga ggc gtg tgt gat gac tgt cag cac aac   1221
Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn
        355                 360                 365

acc atg ggg cgc aac tgt gag cag tgc aag ccg ttt tac tac cag cac   1269
Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His
    370                 375                 380

cca gag agg gac atc cga gat cct aat ttc tgt gaa cga tgt acg tgt   1317
Pro Glu Arg Asp Ile Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys
385                 390                 395                 400

gac cca gct ggc tct caa aat gag gga att tgt gac agc tat act gat   1365
Asp Pro Ala Gly Ser Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp
                405                 410                 415

ttt tct act ggt ctc att gct ggc cag tgt cgg tgt aaa tta aat gtg   1413
Phe Ser Thr Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val
            420                 425                 430

gaa gga gaa cat tgt gat gtt tgc aaa gaa ggc ttc tat gat tta agc   1461
Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser
        435                 440                 445

agt gaa gat cca ttt ggt tgt aaa tct tgt gct tgc aat cct ctg gga   1509
Ser Glu Asp Pro Phe Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly
    450                 455                 460

aca att cct gga ggg aat cct tgt gat tcc gag aca ggt cac tgc tac   1557
Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr
465                 470                 475                 480

tgc aag cgt ctg gtg aca gga cag cat tgt gac cag tgc ctg cca gag   1605
Cys Lys Arg Leu Val Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu
                485                 490                 495

cac tgg ggc tta agc aat gat ttg gat gga tgt cga cca tgt gac tgt   1653
His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys
            500                 505                 510

gac ctt ggg gga gcc tta aac aac agt tgc ttt gcg gag tca ggc cag   1701
Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln
        515                 520                 525

tgc tca tgc cgg cct cac atg att gga cgt cag tgc aac gaa gtg gaa   1749
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Cys Ser Cys Arg Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu
    530                 535                 540

cct ggt tac tac ttt gcc acc ctg gat cac tac ctc tat gaa gcg gag   1797
Pro Gly Tyr Tyr Phe Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu
545                 550                 555                 560

gaa gcc aac ttg ggg cct ggg gtt agc ata gtg gag cgg caa tat atc   1845
Glu Ala Asn Leu Gly Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile
                565                 570                 575

cag gac cgg att ccc tcc tgg act gga gcc ggc ttc gtc cga gtg cct   1893
Gln Asp Arg Ile Pro Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro
            580                 585                 590

gaa ggg gct tat ttg gag ttt ttc att gac aac ata cca tat tcc atg   1941
Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met
        595                 600                 605

gag tac gac atc cta att cgc tac gag cca cag cta ccc gac cac tgg   1989
Glu Tyr Asp Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp
    610                 615                 620

gaa aaa gct gtc atc aca gtg cag cga cct gga agg att cca acc agc   2037
Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser
625                 630                 635                 640

agc cga tgt ggt aat acc atc ccc gat gat gac aac cag gtg gtg tca   2085
Ser Arg Cys Gly Asn Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser
                645                 650                 655

tta tca cca ggc tca aga tat gtc gtc ctt cct cgg ccg gtg tgc ttt   2133
Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe
            660                 665                 670

gag aag gga aca aac tac acg gtg agg ttg gag ctg cct cag tac acc   2181
Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr
        675                 680                 685

tcc tct gat agc gac gtg gag agc ccc tac acg ctg atc gat tct ctt   2229
Ser Ser Asp Ser Asp Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu
    690                 695                 700

gtt ctc atg cca tac tgt aaa tca ctg gac atc ttc acc gtg gga ggt   2277
Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly
705                 710                 715                 720

tca gga gat ggg gtg gtc acc aac agt gcc tgg gaa acc ttt cag aga   2325
Ser Gly Asp Gly Val Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg
                725                 730                 735

tac cga tgt cta gag aac agc aga agc gtt gtg aaa aca ccg atg aca   2373
Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr
            740                 745                 750

gat gtt tgc aga aac atc atc ttt agc att tct gcc ctg tta cac cag   2421
Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln
        755                 760                 765

aca ggc ctg gct tgt gaa tgc gac cct cag ggt tcg tta agt tcc gtg   2469
Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val
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    770                 775                 780

tgt gat ccc aac gga ggc cag tgc cag tgc cgg ccc aac gtg gtt gga   2517
Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly
785                 790                 795                 800

aga acc tgc aac aga tgt gca cct gga act ttt ggc ttt ggc ccc agt   2565
Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser
                805                 810                 815

gga tgc aaa cct tgt gag tgc cat ctg caa gga tct gtc aat gcc ttc   2613
Gly Cys Lys Pro Cys Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe
            820                 825                 830

tgc aat ccc gtc act ggc cag tgc cac tgt ttc cag gga gtg tat gct   2661
Cys Asn Pro Val Thr Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala
        835                 840                 845

cgg cag tgt gat cgg tgc tta cct ggg cac tgg ggc ttt cca agt tgc   2709
Arg Gln Cys Asp Arg Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys
    850                 855                 860

cag ccc tgc cag tgc aat ggc cac gcc gat gac tgc gac cca gtg act   2757
Gln Pro Cys Gln Cys Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr
865                 870                 875                 880

ggg gag tgc ttg aac tgc cag gac tac acc atg ggt cat aac tgt gaa   2805
Gly Glu Cys Leu Asn Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu
                885                 890                 895

agg tgc ttg gct ggt tac tat ggc gac ccc atc att ggg tca ggt gat   2853
Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp
            900                 905                 910

cac tgc cgc cct tgc cct tgc cca gat ggt ccc gac agt gga cgc cag   2901
His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln
        915                 920                 925

ttt gcc agg agc tgc tac caa gat cct gtt act tta cag ctt gcc tgt   2949
Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys
    930                 935                 940

gtt tgt gat cct gga tac att ggt tcc aga tgt gac gac tgt gcc tca   2997
Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser
945                 950                 955                 960

gga tac ttt ggc aat cca tca gaa gtt ggg ggg tcg tgt cag cct tgc   3045
Gly Tyr Phe Gly Asn Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys
                965                 970                 975

cag tgt cac aac aac att gac acg aca gac cca gaa gcc tgt gac aag   3093
Gln Cys His Asn Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys
            980                 985                 990

gag act ggg agg tgt ctc aag tgc ctg tac cac acg gaa ggg gaa cac   3141
Glu Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His
        995                1000                1005

tgt cag ttc tgc cgg ttt gga tac tat ggt gat gcc ctc cgg cag gac   3189
Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp
   1010                1015                1020
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tgt cga aag tgt gtc tgt aat tac ctg ggc acc gtg caa gag cac tgt   3237
Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys
1025              1030                1035                1040

aac ggc tct gac tgc cag tgc gac aaa gcc act ggt cag tgc ttg tgt   3285
Asn Gly Ser Asp Cys Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys
                1045                1050                1055

ctt cct aat gtg atc ggg cag aac tgt gac cgc tgt gcg ccc aat acc   3333
Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr
          1060                1065                1070

tgg cag ctg gcc agt ggc act ggc tgt gac cca tgc aac tgc aat gct   3381
Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala
       1075                1080                1085

gct cat tcc ttc ggg cca tct tgc aat gag ttc acg ggg cag tgc cag   3429
Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln
   1090                1095                1100

tgc atg cct ggg ttt gga ggc cgc acc tgc agc gag tgc cag gaa ctc   3477
Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu
1105                1110                1115                1120

ttc tgg gga gac ccc gac gtg gag tgc cga gcc tgt gac tgt gac ccc   3525
Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro
                1125                1130                1135

agg ggc att gag acg cca cag tgt gac cag tcc acg ggc cag tgt gtc   3573
Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val
          1140                1145                1150

tgc gtt gag ggt gtt gag ggt cca cgc tgt gac aag tgc acg cga ggg   3621
Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly
       1155                1160                1165

tac tcg ggg gtc ttc cct gac tgc aca ccc tgc cac cag tgc ttt gct   3669
Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala
   1170                1175                1180

ctc tgg gat gtg atc att gcc gag ctg acc aac agg aca cac aga ttc   3717
Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe
1185                1190                1195                1200

ctg gag aaa gcc aag gcc ttg aag atc agt ggt gtg atc ggg cct tac   3765
Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr
                1205                1210                1215

cgt gag act gtg gac tcg gtg gag agg aaa gtc agc gag ata aaa gac   3813
Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp
          1220                1225                1230

atc ctg gcg cag agc ccc gca gca gag cca ctg aaa aac att ggg aat   3861
Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn
       1235                1240                1245

ctc ttt gag gaa gca gag aaa ctg att aaa gat gtt aca gaa atg atg   3909
Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met
   1250                1255                1260
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gct caa gta gaa gtg aaa tta tct gac aca act tcc caa agc aac agc   3957
Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser
1265               1270                1275                1280

aca gcc aaa gaa ctg gat tct cta cag aca gaa gcc gaa agc cta gac   4005
Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp
                1285                1290                1295

aac act gtg aaa gaa ctt gct gaa caa ctg gaa ttt atc aaa aac tca   4053
Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser
           1300                1305                1310

gat att cgg ggt gcc ttg gat agc att acc aag tat ttc cag atg tct   4101
Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser
       1315                1320                1325

ctt gag gca gag gag agg gtg aat gcc tcc acc aca gaa ccc aac agc   4149
Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser
   1330                1335                1340

act gtg gag cag tca gcc ctc atg aga gac aga gta gaa gac gtg atg   4197
Thr Val Glu Gln Ser Ala Leu Met Arg Asp Arg Val Glu Asp Val Met
1345               1350                1355                1360

atg gag cga gaa tcc cag ttc aag gaa aaa caa gag gag cag gct cgc   4245
Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg
                1365                1370                1375

ctc ctt gat gaa ctg gca ggc aag cta caa agc cta gac ctt tca gcc   4293
Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala
           1380                1385                1390

gct gcc gaa atg acc tgt gga aca ccc cca ggg gcc tcc tgt tcc gag   4341
Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu
       1395                1400                1405

act gaa tgt ggc ggg cca aac tgc aga act gac gaa gga gag agg aag   4389
Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys
   1410                1415                1420

tgt ggg ggg cct ggc tgt ggt ggt ctg gtt act gtt gca cac aac gcc   4437
Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala
1425               1430                1435                1440

tgg cag aaa gcc atg gac ttg gac caa gat gtc ctg agt gcc ctg gct   4485
Trp Gln Lys Ala Met Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala
                1445                1450                1455

gaa gtg gaa cag ctc tcc aag atg gtc tct gaa gca aaa ctg agg gca   4533
Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala
           1460                1465                1470

gat gag gca aaa caa agt gct gaa gac att ctg ttg aag aca aat gct   4581
Asp Glu Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala
       1475                1480                1485

acc aaa gaa aaa atg gac aag agc aat gag gag ctg aga aat cta atc   4629
Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile
   1490                1495                1500

aag caa atc aga aac ttt ttg acc cag gat agt gct gat ttg gac agc   4677
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Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser
1505                1510                1515                1520

att gaa gca gtt gct aat gaa gta ttg aaa atg gag atg cct agc acc   4725
Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr
                1525                1530                1535

cca cag cag tta cag aac ttg aca gaa gat ata cgt gaa cga gtt gaa   4773
Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu
            1540                1545                1550

agc ctt tct caa gta gag gtt att ctt cag cat agt gct gct gac att   4821
Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile
        1555                1560                1565

gcc aga gct gag atg ttg tta gaa gaa gct aaa aga gca agc aaa agt   4869
Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser
    1570                1575                1580

gca aca gat gtt aaa gtc act gca gat atg gta aag gaa gct ctg gaa   4917
Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu
1585                1590                1595                1600

gaa gca gaa aag gcc cag gtc gca gca gag aag gca att aaa caa gca   4965
Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala
                1605                1610                1615

gat gaa gac att caa gga acc cag aac ctg tta act tcg att gag tct   5013
Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser
            1620                1625                1630

gaa aca gca gct tct gag gaa acc ttg ttc aac gcg tcc cag cgc atc   5061
Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile
        1635                1640                1645

agc gag tta gag agg aat gtg gaa gaa ctt aag cgg aaa gct gcc caa   5109
Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln
    1650                1655                1660

aac tcc ggg gag gca gaa tat att gaa aaa gta gta tat act gtg aag   5157
Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys
1665                1670                1675                1680

caa agt gca gaa gat gtt aag aag act tta gat ggt gaa ctt gat gaa   5205
Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu
                1685                1690                1695

aag tat aaa aaa gta gaa aat tta att gcc aaa aaa act gaa gag tca   5253
Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser
            1700                1705                1710

gct gat gcc aga agg aaa gcc gaa atg cta caa aat gaa gca aaa act   5301
Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr
        1715                1720                1725

ctt tta gct caa gca aat agc aag ctg caa ctg ctc aaa gat tta gaa   5349
Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu
    1730                1735                1740

aga aaa tat gaa gac aat caa aga tac tta gaa gat aaa gct caa gaa   5397
Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu
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1745                1750                1755                1760

tta gca aga ctg gaa gga gaa gtc cgt tca ctc cta aag gat ata agc   5445
Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser
                1765                1770                1775

cag aaa gtt gct gtg tat agc aca tgc ttg taacagagga gaataaaaaa     5495
Gln Lys Val Ala Val Tyr Ser Thr Cys Leu
            1780                1785

tggctgaggt gaacaaggta aaacaactac attttaaaaa ctgacttaat gctcttcaaa 5555

ataaaacatc acctatttaa tgtttttaat cacattttgt atgagttaaa taaagccc   5613
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<210> 14
<211> 1786
<212> PRT
<213> Homo sapiens

<400> 14

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Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Ala Leu Cys Arg
  1               5                  10                  15

Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu
             20                  25                  30

Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln
         35                  40                  45

Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
     50                  55                  60

Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn
 65                  70                  75                  80

Ser Gln Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile
                 85                  90                  95

Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp
            100                 105                 110

Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu
        115                 120                 125

Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg
    130                 135                 140

Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp
145                 150                 155                 160

Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly
                165                 170                 175

Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser
            180                 185                 190

Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg
        195                 200                 205

Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile
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    210                 215                 220

Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu
225                 230                 235                 240

His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu
                245                 250                 255

Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe
            260                 265                 270

Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu
        275                 280                 285

Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr
    290                 295                 300

Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro
305                 310                 315                 320

Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn
                325                 330                 335

Cys Asn Glu His Ser Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu
            340                 345                 350

Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn
        355                 360                 365

Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His
    370                 375                 380

Pro Glu Arg Asp Ile Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys
385                 390                 395                 400

Asp Pro Ala Gly Ser Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp
                405                 410                 415

Phe Ser Thr Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val
            420                 425                 430

Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser
        435                 440                 445

Ser Glu Asp Pro Phe Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly
    450                 455                 460

Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr
465                 470                 475                 480

Cys Lys Arg Leu Val Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu
                485                 490                 495

His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys
            500                 505                 510

Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln
        515                 520                 525

Cys Ser Cys Arg Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu
    530                 535                 540
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Pro Gly Tyr Tyr Phe Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu
545                 550                 555                 560

Glu Ala Asn Leu Gly Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile
                565                 570                 575

Gln Asp Arg Ile Pro Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro
            580                 585                 590

Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met
        595                 600                 605

Glu Tyr Asp Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp
    610                 615                 620

Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser
625                 630                 635                 640

Ser Arg Cys Gly Asn Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser
                645                 650                 655

Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe
            660                 665                 670

Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr
        675                 680                 685

Ser Ser Asp Ser Asp Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu
    690                 695                 700

Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly
705                 710                 715                 720

Ser Gly Asp Gly Val Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg
                725                 730                 735

Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr
            740                 745                 750

Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln
        755                 760                 765

Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val
    770                 775                 780

Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly
785                 790                 795                 800

Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser
                805                 810                 815

Gly Cys Lys Pro Cys Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe
            820                 825                 830

Cys Asn Pro Val Thr Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala
        835                 840                 845

Arg Gln Cys Asp Arg Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys
    850                 855                 860
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Gln Pro Cys Gln Cys Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr
865                 870                 875                 880

Gly Glu Cys Leu Asn Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu
                885                 890                 895

Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp
            900                 905                 910

His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln
        915                 920                 925

Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys
    930                 935                 940

Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser
945                 950                 955                 960

Gly Tyr Phe Gly Asn Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys
                965                 970                 975

Gln Cys His Asn Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys
            980                 985                 990

Glu Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His
        995                1000                1005

Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp
   1010                1015                1020

Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys
1025                1030                1035                1040

Asn Gly Ser Asp Cys Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys
                1045                1050                1055

Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr
            1060                1065                1070

Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala
        1075                1080                1085

Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln
   1090                1095                1100

Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu
1105                1110                1115                1120

Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro
                1125                1130                1135

Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val
            1140                1145                1150

Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly
        1155                1160                1165

Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala
   1170                1175                1180

Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe
```

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1185                1190                1195                1200

Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr
                1205                1210                1215

Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp
            1220                1225                1230

Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn
        1235                1240                1245

Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met
    1250                1255                1260

Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser
1265                1270                1275                1280

Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp
                1285                1290                1295

Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser
            1300                1305                1310

Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser
        1315                1320                1325

Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser
    1330                1335                1340

Thr Val Glu Gln Ser Ala Leu Met Arg Asp Arg Val Glu Asp Val Met
1345                1350                1355                1360

Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg
                1365                1370                1375

Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala
            1380                1385                1390

Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu
        1395                1400                1405

Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys
    1410                1415                1420

Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala
1425                1430                1435                1440

Trp Gln Lys Ala Met Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala
                1445                1450                1455

Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala
            1460                1465                1470

Asp Glu Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala
        1475                1480                1485

Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile
    1490                1495                1500

Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser
1505                1510                1515                1520
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Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr
                1525                1530                1535

Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu
            1540                1545                1550

Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile
        1555                1560                1565

Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser
    1570                1575                1580

Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu
1585                1590                1595                1600

Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala
                1605                1610                1615

Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser
            1620                1625                1630

Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile
        1635                1640                1645

Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln
    1650                1655                1660

Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys
1665                1670                1675                1680

Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu
                1685                1690                1695

Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser
            1700                1705                1710

Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr
        1715                1720                1725

Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu
    1730                1735                1740

Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu
1745                1750                1755                1760

Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser
                1765                1770                1775

Gln Lys Val Ala Val Tyr Ser Thr Cys Leu
            1780                1785
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<400> 15

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Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu Gly Ser Cys Tyr Pro
  1               5                  10                  15

gcc acg ggc gac ctt ctc atc ggc cga gca cag aag ctt tcg gtg acc   96
Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln Lys Leu Ser Val Thr
             20                  25                  30

tcg acg tgc ggg ctg cac aag ccc gaa ccc tac tgt atc gtc agc cac   144
Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr Cys Ile Val Ser His
         35                  40                  45

ttg cag gag gac aaa aaa tgc ttc ata tgc aat tcc caa gat cct tat   192
Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn Ser Gln Asp Pro Tyr
     50                  55                  60

cat gag acc ctg aat cct gac agc cat ctc att gaa aat gtg gtc act   240
His Glu Thr Leu Asn Pro Asp Ser His Leu Ile Glu Asn Val Val Thr
 65                  70                  75                  80

aca ttt gct cca aac cgc ctt aag att tgg tgg caa tct gaa aat ggt   288
Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp Gln Ser Glu Asn Gly
                 85                  90                  95

gtg gaa aat gta act atc caa ctg gat ttg gaa gca gaa ttc cat ttt   336
Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu Ala Glu Phe His Phe
            100                 105                 110

act cat ctc ata atg act ttc aag aca ttc cgt cca gct gct atg ctg   384
Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg Pro Ala Ala Met Leu
        115                 120                 125

ata gaa cga tcg tcc gac ttt ggg aaa acc tgg ggt gtg tat aga tac   432
Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Gly Val Tyr Arg Tyr
    130                 135                 140

ttc gcc tat gac tgt gag gcc tcg ttt cca ggc att tca act ggc ccc   480
Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly Ile Ser Thr Gly Pro
145                 150                 155                 160

atg aaa aaa gtc gat gac ata att tgt gat tct cga tat tct gac att   528
Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser Arg Tyr Ser Asp Ile
                165                 170                 175

gaa ccc tca act gaa gga gag gtg ata ttt cgt gct tta gat cct gct   576
Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg Ala Leu Asp Pro Ala
            180                 185                 190

ttc aaa ata gaa gat cct tat agc cca agg ata cag aat tta tta aaa   624
Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile Gln Asn Leu Leu Lys
        195                 200                 205

att acc aac ttg aga atc aag ttt gtg aaa ctg cat act ttg gga gat   672
Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu His Thr Leu Gly Asp
    210                 215                 220

aac ctt ctg gat tcc agg atg gaa atc aga gaa aag tat tat tat gca   720
Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu Lys Tyr Tyr Tyr Ala
225                 230                 235                 240
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gtt tat gat atg gtg gtt cga gga aat tgc ttc tgc tat ggt cat gcc   768
Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe Cys Tyr Gly His Ala
                245                 250                 255

agc gaa tgt gcc cct gtg gat gga ttc aat gaa gaa gtg gaa gga atg   816
Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu Glu Val Glu Gly Met
            260                 265                 270

gtt cac gga cac tgc atg tgc agg cat aac acc aag ggc tta aac tgt   864
Val His Gly His Cys Met Cys Arg His Asn Thr Lys Gly Leu Asn Cys
        275                 280                 285

gaa ctc tgc atg gat ttc tac cat gat tta cct tgg aga cct gct gaa   912
Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro Trp Arg Pro Ala Glu
    290                 295                 300

ggc cga aac agc aac gcc tgt aaa aaa tgt aac tgc aat gaa cat tcc   960
Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn Cys Asn Glu His Ser
305                 310                 315                 320

atc tct tgt cac ttt gac atg gct gtt tac ctg gcc acg ggg aac gtc   1008
Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu Ala Thr Gly Asn Val
                325                 330                 335

agc gga ggc gtg tgt gat gac tgt cag cac aac acc atg ggg cgc aac   1056
Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn Thr Met Gly Arg Asn
            340                 345                 350

tgt gag cag tgc aag ccg ttt tac tac cag cac cca gag agg gac atc   1104
Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His Pro Glu Arg Asp Ile
        355                 360                 365

cga gat cct aat ttc tgt gaa cga tgt acg tgt gac cca gct ggc tct   1152
Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys Asp Pro Ala Gly Ser
    370                 375                 380

caa aat gag gga att tgt gac agc tat act gat ttt tct act ggt ctc   1200
Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp Phe Ser Thr Gly Leu
385                 390                 395                 400

att gct ggc cag tgt cgg tgt aaa tta aat gtg gaa gga gaa cat tgt   1248
Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val Glu Gly Glu His Cys
                405                 410                 415

gat gtt tgc aaa gaa ggc ttc tat gat tta agc agt gaa gat cca ttt   1296
Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser Ser Glu Asp Pro Phe
            420                 425                 430

ggt tgt aaa tct tgt gct tgc aat cct ctg gga aca att cct gga ggg   1344
Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly Thr Ile Pro Gly Gly
        435                 440                 445

aat cct tgt gat tcc gag aca ggt cac tgc tac tgc aag cgt ctg gtg   1392
Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr Cys Lys Arg Leu Val
    450                 455                 460

aca gga cag cat tgt gac cag tgc ctg cca gag cac tgg ggc tta agc   1440
Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu His Trp Gly Leu Ser
465                 470                 475                 480
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aat gat ttg gat gga tgt cga cca tgt gac tgt gac ctt ggg gga gcc   1488
Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys Asp Leu Gly Gly Ala
                485                 490                 495

tta aac aac agt tgc ttt gcg gag tca ggc cag tgc tca tgc cgg cct   1536
Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln Cys Ser Cys Arg Pro
            500                 505                 510

cac atg att gga cgt cag tgc aac gaa gtg gaa cct ggt tac tac ttt   1584
His Met Ile Gly Arg Gln Cys Asn Glu Val Glu Pro Gly Tyr Tyr Phe
        515                 520                 525

gcc acc ctg gat cac tac ctc tat gaa gcg gag gaa gcc aac ttg ggg   1632
Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu Glu Ala Asn Leu Gly
    530                 535                 540

cct ggg gtt agc ata gtg gag cgg caa tat atc cag gac cgg att ccc   1680
Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile Gln Asp Arg Ile Pro
545                 550                 555                 560

tcc tgg act gga gcc ggc ttc gtc cga gtg cct gaa ggg gct tat ttg   1728
Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro Glu Gly Ala Tyr Leu
                565                 570                 575

gag ttt ttc att gac aac ata cca tat tcc atg gag tac gac atc cta   1776
Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met Glu Tyr Asp Ile Leu
            580                 585                 590

att cgc tac gag cca cag cta ccc gac cac tgg gaa aaa gct gtc atc   1824
Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp Glu Lys Ala Val Ile
        595                 600                 605

aca gtg cag cga cct gga agg att cca acc agc agc cga tgt ggt aat   1872
Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser Ser Arg Cys Gly Asn
    610                 615                 620

acc atc ccc gat gat gac aac cag gtg gtg tca tta tca cca ggc tca   1920
Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser Leu Ser Pro Gly Ser
625                 630                 635                 640

aga tat gtc gtc ctt cct cgg ccg gtg tgc ttt gag aag gga aca aac   1968
Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe Glu Lys Gly Thr Asn
                645                 650                 655

tac acg gtg agg ttg gag ctg cct cag tac acc tcc tct gat agc gac   2016
Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr Ser Ser Asp Ser Asp
            660                 665                 670

gtg gag agc ccc tac acg ctg atc gat tct ctt gtt ctc atg cca tac   2064
Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu Val Leu Met Pro Tyr
        675                 680                 685

tgt aaa tca ctg gac atc ttc acc gtg gga ggt tca gga gat ggg gtg   2112
Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly Ser Gly Asp Gly Val
    690                 695                 700

gtc acc aac agt gcc tgg gaa acc ttt cag aga tac cga tgt cta gag   2160
Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg Tyr Arg Cys Leu Glu
705                 710                 715                 720

aac agc aga agc gtt gtg aaa aca ccg atg aca gat gtt tgc aga aac   2208
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Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr Asp Val Cys Arg Asn
                725                 730                 735

atc atc ttt agc att tct gcc ctg tta cac cag aca ggc ctg gct tgt   2256
Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln Thr Gly Leu Ala Cys
            740                 745                 750

gaa tgc gac cct cag ggt tcg tta agt tcc gtg tgt gat ccc aac gga   2304
Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val Cys Asp Pro Asn Gly
        755                 760                 765

ggc cag tgc cag tgc cgg ccc aac gtg gtt gga aga acc tgc aac aga   2352
Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly Arg Thr Cys Asn Arg
    770                 775                 780

tgt gca cct gga act ttt ggc ttt ggc ccc agt gga tgc aaa cct tgt   2400
Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser Gly Cys Lys Pro Cys
785                 790                 795                 800

gag tgc cat ctg caa gga tct gtc aat gcc ttc tgc aat ccc gtc act   2448
Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe Cys Asn Pro Val Thr
                805                 810                 815

ggc cag tgc cac tgt ttc cag gga gtg tat gct cgg cag tgt gat cgg   2496
Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala Arg Gln Cys Asp Arg
            820                 825                 830

tgc tta cct ggg cac tgg ggc ttt cca agt tgc cag ccc tgc cag tgc   2544
Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys Gln Pro Cys Gln Cys
        835                 840                 845

aat ggc cac gcc gat gac tgc gac cca gtg act ggg gag tgc ttg aac   2592
Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr Gly Glu Cys Leu Asn
    850                 855                 860

tgc cag gac tac acc atg ggt cat aac tgt gaa agg tgc ttg gct ggt   2640
Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu Arg Cys Leu Ala Gly
865                 870                 875                 880

tac tat ggc gac ccc atc att ggg tca ggt gat cac tgc cgc cct tgc   2688
Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp His Cys Arg Pro Cys
                885                 890                 895

cct tgc cca gat ggt ccc gac agt gga cgc cag ttt gcc agg agc tgc   2736
Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln Phe Ala Arg Ser Cys
            900                 905                 910

tac caa gat cct gtt act tta cag ctt gcc tgt gtt tgt gat cct gga   2784
Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys Val Cys Asp Pro Gly
        915                 920                 925

tac att ggt tcc aga tgt gac gac tgt gcc tca gga tac ttt ggc aat   2832
Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser Gly Tyr Phe Gly Asn
    930                 935                 940

cca tca gaa gtt ggg ggg tcg tgt cag cct tgc cag tgt cac aac aac   2880
Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys Gln Cys His Asn Asn
945                 950                 955                 960

att gac acg aca gac cca gaa gcc tgt gac aag gag act ggg agg tgt   2928
Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys Glu Thr Gly Arg Cys
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                965                 970                 975

ctc aag tgc ctg tac cac acg gaa ggg gaa cac tgt cag ttc tgc cgg   2976
Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His Cys Gln Phe Cys Arg
            980                 985                 990

ttt gga tac tat ggt gat gcc ctc cgg cag gac tgt cga aag tgt gtc   3024
Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp Cys Arg Lys Cys Val
        995                1000                1005

tgt aat tac ctg ggc acc gtg caa gag cac tgt aac ggc tct gac tgc   3072
Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys Asn Gly Ser Asp Cys
   1010                1015                1020

cag tgc gac aaa gcc act ggt cag tgc ttg tgt ctt cct aat gtg atc   3120
Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys Leu Pro Asn Val Ile
1025                1030                1035                1040

ggg cag aac tgt gac cgc tgt gcg ccc aat acc tgg cag ctg gcc agt   3168
Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr Trp Gln Leu Ala Ser
                1045                1050                1055

ggc act ggc tgt gac cca tgc aac tgc aat gct gct cat tcc ttc ggg   3216
Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala Ala His Ser Phe Gly
            1060                1065                1070

cca tct tgc aat gag ttc acg ggg cag tgc cag tgc atg cct ggg ttt   3264
Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln Cys Met Pro Gly Phe
        1075                1080                1085

gga ggc cgc acc tgc agc gag tgc cag gaa ctc ttc tgg gga gac ccc   3312
Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu Phe Trp Gly Asp Pro
   1090                1095                1100

gac gtg gag tgc cga gcc tgt gac tgt gac ccc agg ggc att gag acg   3360
Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro Arg Gly Ile Glu Thr
1105                1110                1115                1120

cca cag tgt gac cag tcc acg ggc cag tgt gtc tgc gtt gag ggt gtt   3408
Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val Cys Val Glu Gly Val
                1125                1130                1135

gag ggt cca cgc tgt gac aag tgc acg cga ggg tac tcg ggg gtc ttc   3456
Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly Tyr Ser Gly Val Phe
            1140                1145                1150

cct gac tgc aca ccc tgc cac cag tgc ttt gct ctc tgg gat gtg atc   3504
Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala Leu Trp Asp Val Ile
        1155                1160                1165

att gcc gag ctg acc aac agg aca cac aga ttc ctg gag aaa gcc aag   3552
Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe Leu Glu Lys Ala Lys
   1170                1175                1180

gcc ttg aag atc agt ggt gtg atc ggg cct tac cgt gag act gtg gac   3600
Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr Arg Glu Thr Val Asp
1185                1190                1195                1200

tcg gtg gag agg aaa gtc agc gag ata aaa gac atc ctg gcg cag agc   3648
Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp Ile Leu Ala Gln Ser
                1205                1210                1215
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ccc gca gca gag cca ctg aaa aac att ggg aat ctc ttt gag gaa gca   3696
Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn Leu Phe Glu Glu Ala
          1220                1225                1230

gag aaa ctg att aaa gat gtt aca gaa atg atg gct caa gta gaa gtg   3744
Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met Ala Gln Val Glu Val
       1235                1240                1245

aaa tta tct gac aca act tcc caa agc aac agc aca gcc aaa gaa ctg   3792
Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser Thr Ala Lys Glu Leu
   1250                1255                1260

gat tct cta cag aca gaa gcc gaa agc cta gac aac act gtg aaa gaa   3840
Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp Asn Thr Val Lys Glu
1265                1270                1275                1280

ctt gct gaa caa ctg gaa ttt atc aaa aac tca gat att cgg ggt gcc   3888
Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser Asp Ile Arg Gly Ala
               1285                1290                1295

ttg gat agc att acc aag tat ttc cag atg tct ctt gag gca gag gag   3936
Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser Leu Glu Ala Glu Glu
          1300                1305                1310

agg gtg aat gcc tcc acc aca gaa ccc aac agc act gtg gag cag tca   3984
Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser Thr Val Glu Gln Ser
       1315                1320                1325

gcc ctc atg aga gac aga gta gaa gac gtg atg atg gag cga gaa tcc   4032
Ala Leu Met Arg Asp Arg Val Glu Asp Val Met Met Glu Arg Glu Ser
   1330                1335                1340

cag ttc aag gaa aaa caa gag gag cag gct cgc ctc ctt gat gaa ctg   4080
Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg Leu Leu Asp Glu Leu
1345                1350                1355                1360

gca ggc aag cta caa agc cta gac ctt tca gcc gct gcc gaa atg acc   4128
Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala Ala Ala Glu Met Thr
               1365                1370                1375

tgt gga aca ccc cca ggg gcc tcc tgt tcc gag act gaa tgt ggc ggg   4176
Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu Thr Glu Cys Gly Gly
          1380                1385                1390

cca aac tgc aga act gac gaa gga gag agg aag tgt ggg ggg cct ggc   4224
Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys Cys Gly Gly Pro Gly
       1395                1400                1405

tgt ggt ggt ctg gtt act gtt gca cac aac gcc tgg cag aaa gcc atg   4272
Cys Gly Gly Leu Val Thr Val Ala His Asn Ala Trp Gln Lys Ala Met
   1410                1415                1420

gac ttg gac caa gat gtc ctg agt gcc ctg gct gaa gtg gaa cag ctc   4320
Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala Glu Val Glu Gln Leu
1425                1430                1435                1440

tcc aag atg gtc tct gaa gca aaa ctg agg gca gat gag gca aaa caa   4368
Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala Asp Glu Ala Lys Gln
               1445                1450                1455
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agt gct gaa gac att ctg ttg aag aca aat gct acc aaa gaa aaa atg   4416
Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala Thr Lys Glu Lys Met
          1460                1465                1470

gac aag agc aat gag gag ctg aga aat cta atc aag caa atc aga aac   4464
Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile Lys Gln Ile Arg Asn
       1475                1480                1485

ttt ttg acc cag gat agt gct gat ttg gac agc att gaa gca gtt gct   4512
Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser Ile Glu Ala Val Ala
   1490                1495                1500

aat gaa gta ttg aaa atg gag atg cct agc acc cca cag cag tta cag   4560
Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr Pro Gln Gln Leu Gln
1505                1510                1515                1520

aac ttg aca gaa gat ata cgt gaa cga gtt gaa agc ctt tct caa gta   4608
Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu Ser Leu Ser Gln Val
               1525                1530                1535

gag gtt att ctt cag cat agt gct gct gac att gcc aga gct gag atg   4656
Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile Ala Arg Ala Glu Met
          1540                1545                1550

ttg tta gaa gaa gct aaa aga gca agc aaa agt gca aca gat gtt aaa   4704
Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser Ala Thr Asp Val Lys
       1555                1560                1565

gtc act gca gat atg gta aag gaa gct ctg gaa gaa gca gaa aag gcc   4752
Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu Glu Ala Glu Lys Ala
   1570                1575                1580

cag gtc gca gca gag aag gca att aaa caa gca gat gaa gac att caa   4800
Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala Asp Glu Asp Ile Gln
1585                1590                1595                1600

gga acc cag aac ctg tta act tcg att gag tct gaa aca gca gct tct   4848
Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser Glu Thr Ala Ala Ser
               1605                1610                1615

gag gaa acc ttg ttc aac gcg tcc cag cgc atc agc gag tta gag agg   4896
Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile Ser Glu Leu Glu Arg
          1620                1625                1630

aat gtg gaa gaa ctt aag cgg aaa gct gcc caa aac tcc ggg gag gca   4944
Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln Asn Ser Gly Glu Ala
       1635                1640                1645

gaa tat att gaa aaa gta gta tat act gtg aag caa agt gca gaa gat   4992
Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys Gln Ser Ala Glu Asp
   1650                1655                1660

gtt aag aag act tta gat ggt gaa ctt gat gaa aag tat aaa aaa gta   5040
Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu Lys Tyr Lys Lys Val
1665                1670                1675                1680

gaa aat tta att gcc aaa aaa act gaa gag tca gct gat gcc aga agg   5088
Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser Ala Asp Ala Arg Arg
               1685                1690                1695

aaa gcc gaa atg cta caa aat gaa gca aaa act ctt tta gct caa gca   5136
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Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr Leu Leu Ala Gln Ala
          1700                1705                1710

aat agc aag ctg caa ctg ctc aaa gat tta gaa aga aaa tat gaa gac   5184
Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu Arg Lys Tyr Glu Asp
       1715                1720                1725

aat caa aga tac tta gaa gat aaa gct caa gaa tta gca aga ctg gaa   5232
Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu Leu Ala Arg Leu Glu
   1730                1735                1740

gga gaa gtc cgt tca ctc cta aag gat ata agc cag aaa gtt gct gtg   5280
Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser Gln Lys Val Ala Val
1745                1750                1755                1760

tat agc aca tgc ttg taacagagga gaataaaaaa tggctgaggt gaacaaggta   5335
Tyr Ser Thr Cys Leu
                1765

aaacaactac attttaaaaa ctgacttaat gctcttcaaa ataaaacatc acctatttaa 5395

tgtttttaat cacattttgt atgagttaaa taaagccc                         5433


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Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln Lys Leu Ser Val Thr
             20                  25                  30

Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr Cys Ile Val Ser His
         35                  40                  45

Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asn Ser Gln Asp Pro Tyr
     50                  55                  60

His Glu Thr Leu Asn Pro Asp Ser His Leu Ile Glu Asn Val Val Thr
 65                  70                  75                  80

Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp Gln Ser Glu Asn Gly
                 85                  90                  95

Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu Ala Glu Phe His Phe
            100                 105                 110

Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg Pro Ala Ala Met Leu
        115                 120                 125

Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp Gly Val Tyr Arg Tyr
    130                 135                 140

Phe Ala Tyr Asp Cys Glu Ala Ser Phe Pro Gly Ile Ser Thr Gly Pro
145                 150                 155                 160

Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser Arg Tyr Ser Asp Ile
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                165                 170                 175

Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg Ala Leu Asp Pro Ala
            180                 185                 190

Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile Gln Asn Leu Leu Lys
        195                 200                 205

Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu His Thr Leu Gly Asp
    210                 215                 220

Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu Lys Tyr Tyr Tyr Ala
225                 230                 235                 240

Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe Cys Tyr Gly His Ala
                245                 250                 255

Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu Glu Val Glu Gly Met
            260                 265                 270

Val His Gly His Cys Met Cys Arg His Asn Thr Lys Gly Leu Asn Cys
        275                 280                 285

Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro Trp Arg Pro Ala Glu
    290                 295                 300

Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn Cys Asn Glu His Ser
305                 310                 315                 320

Ile Ser Cys His Phe Asp Met Ala Val Tyr Leu Ala Thr Gly Asn Val
                325                 330                 335

Ser Gly Gly Val Cys Asp Asp Cys Gln His Asn Thr Met Gly Arg Asn
            340                 345                 350

Cys Glu Gln Cys Lys Pro Phe Tyr Tyr Gln His Pro Glu Arg Asp Ile
        355                 360                 365

Arg Asp Pro Asn Phe Cys Glu Arg Cys Thr Cys Asp Pro Ala Gly Ser
    370                 375                 380

Gln Asn Glu Gly Ile Cys Asp Ser Tyr Thr Asp Phe Ser Thr Gly Leu
385                 390                 395                 400

Ile Ala Gly Gln Cys Arg Cys Lys Leu Asn Val Glu Gly Glu His Cys
                405                 410                 415

Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser Ser Glu Asp Pro Phe
            420                 425                 430

Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly Thr Ile Pro Gly Gly
        435                 440                 445

Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr Cys Lys Arg Leu Val
    450                 455                 460

Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu His Trp Gly Leu Ser
465                 470                 475                 480

Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys Asp Leu Gly Gly Ala
                485                 490                 495
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Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln Cys Ser Cys Arg Pro
            500                 505                 510

His Met Ile Gly Arg Gln Cys Asn Glu Val Glu Pro Gly Tyr Tyr Phe
        515                 520                 525

Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu Glu Ala Asn Leu Gly
    530                 535                 540

Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile Gln Asp Arg Ile Pro
545                 550                 555                 560

Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro Glu Gly Ala Tyr Leu
                565                 570                 575

Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met Glu Tyr Asp Ile Leu
            580                 585                 590

Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp Glu Lys Ala Val Ile
        595                 600                 605

Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser Ser Arg Cys Gly Asn
    610                 615                 620

Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser Leu Ser Pro Gly Ser
625                 630                 635                 640

Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe Glu Lys Gly Thr Asn
                645                 650                 655

Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr Ser Ser Asp Ser Asp
            660                 665                 670

Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu Val Leu Met Pro Tyr
        675                 680                 685

Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly Ser Gly Asp Gly Val
    690                 695                 700

Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg Tyr Arg Cys Leu Glu
705                 710                 715                 720

Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr Asp Val Cys Arg Asn
                725                 730                 735

Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln Thr Gly Leu Ala Cys
            740                 745                 750

Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val Cys Asp Pro Asn Gly
        755                 760                 765

Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly Arg Thr Cys Asn Arg
    770                 775                 780

Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser Gly Cys Lys Pro Cys
785                 790                 795                 800

Glu Cys His Leu Gln Gly Ser Val Asn Ala Phe Cys Asn Pro Val Thr
                805                 810                 815
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Gly Gln Cys His Cys Phe Gln Gly Val Tyr Ala Arg Gln Cys Asp Arg
            820                 825                 830

Cys Leu Pro Gly His Trp Gly Phe Pro Ser Cys Gln Pro Cys Gln Cys
        835                 840                 845

Asn Gly His Ala Asp Asp Cys Asp Pro Val Thr Gly Glu Cys Leu Asn
    850                 855                 860

Cys Gln Asp Tyr Thr Met Gly His Asn Cys Glu Arg Cys Leu Ala Gly
865                 870                 875                 880

Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp His Cys Arg Pro Cys
                885                 890                 895

Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln Phe Ala Arg Ser Cys
            900                 905                 910

Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys Val Cys Asp Pro Gly
        915                 920                 925

Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser Gly Tyr Phe Gly Asn
    930                 935                 940

Pro Ser Glu Val Gly Gly Ser Cys Gln Pro Cys Gln Cys His Asn Asn
945                 950                 955                 960

Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys Glu Thr Gly Arg Cys
                965                 970                 975

Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His Cys Gln Phe Cys Arg
            980                 985                 990

Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp Cys Arg Lys Cys Val
        995                1000                1005

Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys Asn Gly Ser Asp Cys
   1010                1015                1020

Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys Leu Pro Asn Val Ile
1025                1030                1035                1040

Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr Trp Gln Leu Ala Ser
                1045                1050                1055

Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala Ala His Ser Phe Gly
            1060                1065                1070

Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln Cys Met Pro Gly Phe
        1075                1080                1085

Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu Phe Trp Gly Asp Pro
   1090                1095                1100

Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro Arg Gly Ile Glu Thr
1105                1110                1115                1120

Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val Cys Val Glu Gly Val
                1125                1130                1135

Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly Tyr Ser Gly Val Phe
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          1140                1145                1150

Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala Leu Trp Asp Val Ile
       1155                1160                1165

Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe Leu Glu Lys Ala Lys
   1170                1175                1180

Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr Arg Glu Thr Val Asp
1185                1190                1195                1200

Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp Ile Leu Ala Gln Ser
                1205                1210                1215

Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn Leu Phe Glu Glu Ala
           1220                1225                1230

Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met Ala Gln Val Glu Val
       1235                1240                1245

Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser Thr Ala Lys Glu Leu
   1250                1255                1260

Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp Asn Thr Val Lys Glu
1265                1270                1275                1280

Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser Asp Ile Arg Gly Ala
                1285                1290                1295

Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser Leu Glu Ala Glu Glu
           1300                1305                1310

Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser Thr Val Glu Gln Ser
       1315                1320                1325

Ala Leu Met Arg Asp Arg Val Glu Asp Val Met Met Glu Arg Glu Ser
   1330                1335                1340

Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg Leu Leu Asp Glu Leu
1345                1350                1355                1360

Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala Ala Ala Glu Met Thr
                1365                1370                1375

Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu Thr Glu Cys Gly Gly
           1380                1385                1390

Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys Cys Gly Gly Pro Gly
       1395                1400                1405

Cys Gly Gly Leu Val Thr Val Ala His Asn Ala Trp Gln Lys Ala Met
   1410                1415                1420

Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala Glu Val Glu Gln Leu
1425                1430                1435                1440

Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala Asp Glu Ala Lys Gln
                1445                1450                1455

Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala Thr Lys Glu Lys Met
           1460                1465                1470
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Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile Lys Gln Ile Arg Asn
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Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser Ile Glu Ala Val Ala
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Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr Pro Gln Gln Leu Gln
1505                1510                1515                1520

Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu Ser Leu Ser Gln Val
                1525                1530                1535

Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile Ala Arg Ala Glu Met
            1540                1545                1550

Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser Ala Thr Asp Val Lys
       1555                1560                1565

Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu Glu Ala Glu Lys Ala
   1570                1575                1580

Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala Asp Glu Asp Ile Gln
1585                1590                1595                1600

Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser Glu Thr Ala Ala Ser
                1605                1610                1615

Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile Ser Glu Leu Glu Arg
            1620                1625                1630

Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln Asn Ser Gly Glu Ala
       1635                1640                1645

Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys Gln Ser Ala Glu Asp
   1650                1655                1660

Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu Lys Tyr Lys Lys Val
1665                1670                1675                1680

Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser Ala Asp Ala Arg Arg
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Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr Leu Leu Ala Gln Ala
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Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu Arg Lys Tyr Glu Asp
       1715                1720                1725

Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu Leu Ala Arg Leu Glu
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Tyr Ser Thr Cys Leu
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gcttgcctgc tgcgtcctcc ttcccgtgcc gcgtcccctc gtctgcgagg actggac 177

atg ggg ctg ctc cag gtg ttc gcc ttt ggt gtc cta gcc cta tgg ggc 225
Met Gly Leu Leu Gln Val Phe Ala Phe Gly Val Leu Ala Leu Trp Gly
1 5 10 15

acc cga gtg tgc gct cag gaa ccg gag ttc agc tat ggc tgc gca gaa 273
Thr Arg Val Cys Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu
20 25 30

ggc agc tgc tac cct gcc act ggc gac ctt ctc atc ggc cga gcg caa 321
Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln
35 40 45

aag ctc tcc gtg act tcg aca tgt gga ctg cac aaa cca gag ccc tac 369
Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
50 55 60

tgt att gtt agc cac ctg cag gag gac aag aaa tgc ttc ata tgt gac 417
Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asp
65 70 75 80

tcc cga gac cct tat cac gag acc ctc aac ccc gac agc cat ctc att 465
Ser Arg Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile
85 90 95

gag aac gtg gtc acc aca ttt gct cca aac cgc ctt aag atc tgg tgg 513
Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp
100 105 110

caa tcg gaa aat ggt gtg gag aac gtg acc atc caa ctg gac ctg gaa 561
Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu
115 120 125

gca gaa ttc cat ttc act cat ctc atc atg acc ttc aag aca ttc cgc 609
Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg
130 135 140

cca gcc gcc atg ctg atc gag cgg tct tct gac ttt ggg aag act tgg 657
Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp
145 150 155 160

ggc gtg tac aga tac ttc gcc tac gac tgt gag agc tcg ttc cca ggc 705
Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ser Ser Phe Pro Gly
165 170 175

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att tca act gga ccc atg aag aaa gtg gat gac atc atc tgt gac tct   753
Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser
            180                 185                 190

cga tat tct gac att gag ccc tcg aca gaa gga gag gta ata ttt cgt   801
Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg
        195                 200                 205

gct tta gat cct gct ttc aaa att gaa gac cct tat agt cca agg ata   849
Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile
    210                 215                 220

cag aat cta tta aaa atc acc aac ttg aga atc aag ttt gtg aaa ctg   897
Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu
225                 230                 235                 240

cac acc ttg ggg gat aac ctt ttg gac tcc aga atg gaa atc cga gag   945
His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu
                245                 250                 255

aag tac tat tac gct gtt tat gat atg gtg gtt cga ggg aac tgc ttc   993
Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe
            260                 265                 270

tgc tat ggc cac gcc agt gaa tgc gcc cct gtg gat gga gtc aat gaa   1041
Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Val Asn Glu
        275                 280                 285

gaa gtg gaa gga atg gtt cac ggg cac tgc atg tgc aga cac aac acc   1089
Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr
    290                 295                 300

aaa ggc ctg aac tgt gag ctg tgc atg gat ttc tac cac gat ttg ccg   1137
Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro
305                 310                 315                 320

tgg aga cct gct gaa ggc cgg aac agc aac gcc tgc aaa aaa tgt aac   1185
Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn
                325                 330                 335

tgc aat gaa cat tcc agc tcg tgt cac ttt gac atg gca gtc ttc ctg   1233
Cys Asn Glu His Ser Ser Ser Cys His Phe Asp Met Ala Val Phe Leu
            340                 345                 350

gct act ggc aac gtc agc ggg gga gtg tgt gat aac tgt cag cac aac   1281
Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asn Cys Gln His Asn
        355                 360                 365

acc atg ggg cgc aac tgt gaa cag tgc aaa ccg ttc tac ttc cag cac   1329
Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Phe Gln His
    370                 375                 380

cct gag agg gac atc cgg gac ccc aat ctc tgt gaa cca tgt acc tgt   1377
Pro Glu Arg Asp Ile Arg Asp Pro Asn Leu Cys Glu Pro Cys Thr Cys
385                 390                 395                 400

gac cca gct ggt tct gag aat ggc ggg atc tgt gat ggg tac act gat   1425
Asp Pro Ala Gly Ser Glu Asn Gly Gly Ile Cys Asp Gly Tyr Thr Asp
                405                 410                 415
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ttt tct gtg ggt ctc att gct ggt cag tgt cgg tgc aaa ttg cac gtg   1473
Phe Ser Val Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu His Val
            420                 425                 430

gag gga gag cgc tgt gat gtt tgt aaa gaa ggc ttc tac gac tta agt   1521
Glu Gly Glu Arg Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser
        435                 440                 445

gct gaa gac ccg tat ggt tgt aaa tca tgt gct tgc aat cct ctg gga   1569
Ala Glu Asp Pro Tyr Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly
    450                 455                 460

aca att cct ggt ggg aat cct tgt gat tct gag act ggc tac tgc tac   1617
Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly Tyr Cys Tyr
465                 470                 475                 480

tgt aag cgc ctg gtg aca gga cag cgc tgt gac cag tgc ctg ccg cag   1665
Cys Lys Arg Leu Val Thr Gly Gln Arg Cys Asp Gln Cys Leu Pro Gln
                485                 490                 495

cac tgg ggt tta agc aat gat ttg gat ggg tgt cga cct tgt gac tgt   1713
His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys
            500                 505                 510

gac ctt gga ggg gcg ctg aac aat agc tgc tcc gag gac tcc ggc cag   1761
Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Ser Glu Asp Ser Gly Gln
        515                 520                 525

tgc tcc tgc ctg ccc cac atg att ggg cgg cag tgt aac gag gtg gag   1809
Cys Ser Cys Leu Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu
    530                 535                 540

tcc ggt tac tac ttc acc acc ctg gac cac tac atc tac gaa gcc gag   1857
Ser Gly Tyr Tyr Phe Thr Thr Leu Asp His Tyr Ile Tyr Glu Ala Glu
545                 550                 555                 560

gaa gcc aat ctg ggg cct gga gtc gtt gtg gtg gaa agg cag tac att   1905
Glu Ala Asn Leu Gly Pro Gly Val Val Val Val Glu Arg Gln Tyr Ile
                565                 570                 575

cag gac cgc att cct tcc tgg aca gga cct ggc ttc gtc cgg gtg cct   1953
Gln Asp Arg Ile Pro Ser Trp Thr Gly Pro Gly Phe Val Arg Val Pro
            580                 585                 590

gaa ggg gct tat ttg gag ttt ttc att gac aac ata cca tat tcc atg   2001
Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met
        595                 600                 605

gag tat gaa atc ctg att cgc tat gag cca cag ctg ccg gac cac tgg   2049
Glu Tyr Glu Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp
    610                 615                 620

gag aaa gct gtc atc act gta cag cgg ccg ggg aag att cca gcc agc   2097
Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Lys Ile Pro Ala Ser
625                 630                 635                 640

agc cga tgt ggt aac acc gtt ccc gat gat gac aac cag gtg gtg tcc   2145
Ser Arg Cys Gly Asn Thr Val Pro Asp Asp Asp Asn Gln Val Val Ser
                645                 650                 655

ttg tca ccg ggc tca aga tac gtt gtc ctc cct cgc ccc gtg tgc ttt   2193
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Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe
            660                 665                 670

gag aag gga atg aac tac acg gtg agg ttg gag ctg ccc cag tat acg   2241
Glu Lys Gly Met Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr
        675                 680                 685

gca tcg ggc agt gac gtg gag agc cct tac acg ttc atc gac tcg ctt   2289
Ala Ser Gly Ser Asp Val Glu Ser Pro Tyr Thr Phe Ile Asp Ser Leu
    690                 695                 700

gtt ctc atg ccc tac tgt aaa tcg ctg gac atc ttc act gtt ggc ggc   2337
Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly
705                 710                 715                 720

tca ggc gat ggg gag gtc acc aat agt gcc tgg gaa acc ttc cag cgc   2385
Ser Gly Asp Gly Glu Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg
                725                 730                 735

tac agg tgt ctg gag aac agc agg agt gtg gta aaa aca ccc atg aca   2433
Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr
            740                 745                 750

gat gtc tgc aga aac att atc ttc agc att tct gcc ttg att cac cag   2481
Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Ile His Gln
        755                 760                 765

acg ggc ctt gct tgt gaa tgt gac ccc cag gga tct ctg agt tct gtg   2529
Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val
    770                 775                 780

tgt gac ccc aat ggt ggc cag tgc cag tgc cgt cct aat gtg gtt gga   2577
Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly
785                 790                 795                 800

aga acc tgc aac agg tgt gcc ccg ggc acc ttt ggc ttt ggc ccc aac   2625
Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Asn
                805                 810                 815

gga tgc aaa cct tgt gac tgc cat ctg caa ggg tct gcc agt gcc ttc   2673
Gly Cys Lys Pro Cys Asp Cys His Leu Gln Gly Ser Ala Ser Ala Phe
            820                 825                 830

tgc gat gcg atc act ggc cag tgc cac tgt ttc cag ggc atc tat gct   2721
Cys Asp Ala Ile Thr Gly Gln Cys His Cys Phe Gln Gly Ile Tyr Ala
        835                 840                 845

cgg cag tgt gac cga tgt ctc cct ggg tat tgg ggc ttt ccc agc tgc   2769
Arg Gln Cys Asp Arg Cys Leu Pro Gly Tyr Trp Gly Phe Pro Ser Cys
    850                 855                 860

cag ccc tgc cag tgt aat ggt cat gct cta gac tgt gac aca gtg aca   2817
Gln Pro Cys Gln Cys Asn Gly His Ala Leu Asp Cys Asp Thr Val Thr
865                 870                 875                 880

ggg gag tgt ctg agc tgt cag gac tac acc acg ggc cac aac tgc gaa   2865
Gly Glu Cys Leu Ser Cys Gln Asp Tyr Thr Thr Gly His Asn Cys Glu
                885                 890                 895

agg tgc ctg gct ggc tac tac ggt gat ccc atc att ggg tca gga gac   2913
Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp
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           900                 905                 910

cac tgt cgc cct tgc cct tgt cct gat ggt cct gac agt gga cga cag   2961
His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln
        915                 920                 925

ttt gcc agg agc tgt tat caa gac ccc gtc act ctc cag ctt gcg tgt   3009
Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys
    930                 935                 940

gtt tgt gat cct ggg tac att ggc tcc aga tgt gat gac tgt gcc tct   3057
Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser
945                 950                 955                 960

gga ttt ttt ggc aat ccc tca gac ttt ggg ggt tca tgt caa ccg tgt   3105
Gly Phe Phe Gly Asn Pro Ser Asp Phe Gly Gly Ser Cys Gln Pro Cys
                965                 970                 975

cag tgc cac cac aac att gac act acc gat cca gaa gcc tgt gac aag   3153
Gln Cys His His Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys
            980                 985                 990

gac acg gga cga tgc ctc aag tgc ctg tac cac acg gaa ggg gac cat   3201
Asp Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Asp His
        995                1000                1005

tgc cag ctc tgc cag tat ggg tac tac ggc gat gct ctt cgg caa gac   3249
Cys Gln Leu Cys Gln Tyr Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp
   1010                1015                1020

tgt aga aag tgt gtc tgc aat tac ctg ggc acg gtg aag gaa cat tgt   3297
Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Lys Glu His Cys
1025                1030                1035                1040

aat ggc tct gac tgc cac tgt gac aaa gcc act ggt cag tgc tcg tgc   3345
Asn Gly Ser Asp Cys His Cys Asp Lys Ala Thr Gly Gln Cys Ser Cys
               1045                1050                1055

ctt ccc aat gtg atc ggg cag aac tgt gac cgg tgt gcg ccc aac acc   3393
Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr
           1060                1065                1070

tgg cag ctg gct agc ggg act ggc tgc ggg ccc tgc aat tgc aat gct   3441
Trp Gln Leu Ala Ser Gly Thr Gly Cys Gly Pro Cys Asn Cys Asn Ala
       1075                1080                1085

gcg cat tcc ttt ggg cca tcc tgc aac gag ttc aca ggg cag tgc cag   3489
Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln
   1090                1095                1100

tgc atg ccg ggc ttt gga ggc cga acc tgc agc gag tgc cag gag ctc   3537
Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu
1105                1110                1115                1120

ttc tgg gga gac cct gat gtg gaa tgc cga gcc tgt gac tgt gat ccc   3585
Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro
               1125                1130                1135

agg ggc att gag aca cct cag tgt gac cag tcc acg ggc cag tgt gtc   3633
Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val
           1140                1145                1150
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tgt gtg gag ggt gta gag ggt cct cgc tgc gac aag tgc acc aga ggt   3681
Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly
       1155                1160                1165

tac tcg ggg gtc ttt cct gac tgc aca ccc tgc cac cag tgc ttt gct   3729
Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala
   1170                1175                1180

ctc tgg gat gct atc att ggt gag ctg acc aac agg acc cac aaa ttc   3777
Leu Trp Asp Ala Ile Ile Gly Glu Leu Thr Asn Arg Thr His Lys Phe
1185                1190                1195                1200

ctg gag aaa gcc aag gct ctg aaa atc agt ggt gtg att ggt ccc tac   3825
Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr
               1205                1210                1215

cga gag acc gtg gac tct gta gag aag aaa gtc aat gag ata aaa gac   3873
Arg Glu Thr Val Asp Ser Val Glu Lys Lys Val Asn Glu Ile Lys Asp
          1220                1225                1230

atc ctg gcc cag agc cca gca gcg gaa cca ctg aaa aac att ggc att   3921
Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Ile
       1235                1240                1245

ctc ttc gag gag gca gag aaa cta acc aaa gat gtc aca gaa aag atg   3969
Leu Phe Glu Glu Ala Glu Lys Leu Thr Lys Asp Val Thr Glu Lys Met
   1250                1255                1260

gcg cag gta gaa gtg aaa tta act gat aca gct tca cag agt aac agc   4017
Ala Gln Val Glu Val Lys Leu Thr Asp Thr Ala Ser Gln Ser Asn Ser
1265                1270                1275                1280

aca gct gga gag ctc ggc gca ctg cag gca gaa gca gag agc ctt gac   4065
Thr Ala Gly Glu Leu Gly Ala Leu Gln Ala Glu Ala Glu Ser Leu Asp
               1285                1290                1295

aag acc gtg aag gag ctg gca gaa cag ctg gag ttt atc aaa aac tcc   4113
Lys Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser
          1300                1305                1310

gat att cag ggc gcc ttg gat agc atc acc aag tat ttc cag atg tct   4161
Asp Ile Gln Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser
       1315                1320                1325

ctt gag gca gag aag cgg gtg aat gcc tcc acc aca gac ccc aac agc   4209
Leu Glu Ala Glu Lys Arg Val Asn Ala Ser Thr Thr Asp Pro Asn Ser
   1330                1335                1340

act gtg gag cag tct gcc ctc acg cga gac aga gta gaa gat ctg atg   4257
Thr Val Glu Gln Ser Ala Leu Thr Arg Asp Arg Val Glu Asp Leu Met
1345                1350                1355                1360

ttg gag cga gag tct ccg ttc aag gag cag cag gag gaa cag gca cgc   4305
Leu Glu Arg Glu Ser Pro Phe Lys Glu Gln Gln Glu Glu Gln Ala Arg
               1365                1370                1375

ctc ctg gac gaa ctg gcc ggc aaa ctg caa agt ctc gac ctg tcg gct   4353
Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala
          1380                1385                1390
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gct gca cag atg acc tgt gga aca cct cca ggg gct gac tgt tct gaa   4401
Ala Ala Gln Met Thr Cys Gly Thr Pro Pro Gly Ala Asp Cys Ser Glu
       1395                1400                1405

agt gaa tgt ggt ggc ccc aac tgc aga act gac gaa gga gag aag aag   4449
Ser Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Lys Lys
   1410                1415                1420

tgt ggg ggg cct ggc tgt ggt ggt ctg gtc act gtg gcc cac agt gct   4497
Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Ser Ala
1425                1430                1435                1440

tgg cag aaa gcc atg gat ttt gac cgt gat gtc ctg agt gcc ctg gct   4545
Trp Gln Lys Ala Met Asp Phe Asp Arg Asp Val Leu Ser Ala Leu Ala
                1445                1450                1455

gaa gtc gaa cag ctc tcc aag atg gtc tct gaa gca aaa gtg aga gca   4593
Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Val Arg Ala
           1460                1465                1470

gat gag gcg aag cag aat gcg cag gat gtc ctg tta aaa aca aat gct   4641
Asp Glu Ala Lys Gln Asn Ala Gln Asp Val Leu Leu Lys Thr Asn Ala
       1475                1480                1485

acc aaa gaa aaa gtg gac aag agc aac gag gac ctg cgg aac ctc atc   4689
Thr Lys Glu Lys Val Asp Lys Ser Asn Glu Asp Leu Arg Asn Leu Ile
   1490                1495                1500

aag cag atc aga aac ttc ctg act gag gat agt gct gat cta gac agt   4737
Lys Gln Ile Arg Asn Phe Leu Thr Glu Asp Ser Ala Asp Leu Asp Ser
1505                1510                1515                1520

att gaa gca gtt gct aat gaa gta ctg aaa agt gga aat gct agc acg   4785
Ile Glu Ala Val Ala Asn Glu Val Leu Lys Ser Gly Asn Ala Ser Thr
                1525                1530                1535

cca cag cag tta cag aac cta aca gaa gac att cgg gag cga gtt gaa   4833
Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu
           1540                1545                1550

acc ctc tct caa gta gag gtt att ttg cag cag agt gca gct gac att   4881
Thr Leu Ser Gln Val Glu Val Ile Leu Gln Gln Ser Ala Ala Asp Ile
       1555                1560                1565

gcc aga gct gag ctg ttg ctt gag gaa gct aag aga gca agc aaa agt   4929
Ala Arg Ala Glu Leu Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser
   1570                1575                1580

gca aca gat gtt aaa gtc act gca gac atg gtg aag gaa gca tta gaa   4977
Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu
1585                1590                1595                1600

gaa gca gaa aag gcc cag gtt gca gca gag aag gcg att aaa caa gct   5025
Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala
                1605                1610                1615

gat gag gat atc caa gga acc caa aac ctg cta aca tcg att gaa tct   5073
Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser
           1620                1625                1630

gaa acg gca gct tct gag gaa acc ctg acc aac gcc tcc cag cgc atc   5121
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Glu Thr Ala Ala Ser Glu Glu Thr Leu Thr Asn Ala Ser Gln Arg Ile
       1635                1640                1645

agc aag ctt gag agg aac gtg gaa gag ctt aag cgt aaa gct gcc cag   5169
Ser Lys Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln
   1650                1655                1660

aac tct ggg gag gca gaa tat atc gaa aaa gta gta tat tct gta aaa   5217
Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Ser Val Lys
1665                1670                1675                1680

cag aat gca gac gat gtt aaa aag act cta gat ggc gaa ctt gat gaa   5265
Gln Asn Ala Asp Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu
               1685                1690                1695

aag tat aag aag gta gaa agt tta att gcc caa aaa act gaa gag tca   5313
Lys Tyr Lys Lys Val Glu Ser Leu Ile Ala Gln Lys Thr Glu Glu Ser
           1700                1705                1710

gca gat gcc agg agg aaa gct gag ctg cta caa aat gaa gca aaa aca   5361
Ala Asp Ala Arg Arg Lys Ala Glu Leu Leu Gln Asn Glu Ala Lys Thr
       1715                1720                1725

ctc ttg gct caa gct aac agc aag ctc cag ctg ttg gaa gac tta gaa   5409
Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Glu Asp Leu Glu
   1730                1735                1740

aga aaa tat gag gac aat caa aaa tac tta gaa gat aaa gct caa gaa   5457
Arg Lys Tyr Glu Asp Asn Gln Lys Tyr Leu Glu Asp Lys Ala Gln Glu
1745                1750                1755                1760

ttg gtg cga ctg gaa gga gag gtt cgc tcc ctc ctt aag gac ata agt   5505
Leu Val Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser
               1765                1770                1775

gag aaa gtt gcg gtt tac agc acc tgc tta taacaggaag gggctgtaga     5555
Glu Lys Val Ala Val Tyr Ser Thr Cys Leu
           1780                1785

ggggctcggt gaccaaggta aaccacacgc gcaaaccgag gcagtcatct acaaataacc 5615

catcatctat ttaatgtttt taaccaccta cttttgtatg gagttaaata aaagacattg 5675

gttttgtata aaca                                                   5689


<210> 18
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  1               5                  10                  15

Thr Arg Val Cys Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu
             20                  25                  30

Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln
         35                  40                  45
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Lys Leu Ser Val Thr Ser Thr Cys Gly Leu His Lys Pro Glu Pro Tyr
     50                  55                  60

Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe Ile Cys Asp
 65                  70                  75                  80

Ser Arg Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser His Leu Ile
                 85                  90                  95

Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys Ile Trp Trp
            100                 105                 110

Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu Asp Leu Glu
        115                 120                 125

Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys Thr Phe Arg
    130                 135                 140

Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly Lys Thr Trp
145                 150                 155                 160

Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ser Ser Phe Pro Gly
                165                 170                 175

Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile Cys Asp Ser
            180                 185                 190

Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val Ile Phe Arg
        195                 200                 205

Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser Pro Arg Ile
    210                 215                 220

Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu
225                 230                 235                 240

His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu Ile Arg Glu
                245                 250                 255

Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe
            260                 265                 270

Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Val Asn Glu
        275                 280                 285

Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr
    290                 295                 300

Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro
305                 310                 315                 320

Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys Lys Cys Asn
                325                 330                 335

Cys Asn Glu His Ser Ser Ser Cys His Phe Asp Met Ala Val Phe Leu
            340                 345                 350

Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asn Cys Gln His Asn
        355                 360                 365

Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr Phe Gln His
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    370                 375                 380

Pro Glu Arg Asp Ile Arg Asp Pro Asn Leu Cys Glu Pro Cys Thr Cys
385                 390                 395                 400

Asp Pro Ala Gly Ser Glu Asn Gly Gly Ile Cys Asp Gly Tyr Thr Asp
                405                 410                 415

Phe Ser Val Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys Leu His Val
            420                 425                 430

Glu Gly Glu Arg Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser
        435                 440                 445

Ala Glu Asp Pro Tyr Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly
    450                 455                 460

Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly Tyr Cys Tyr
465                 470                 475                 480

Cys Lys Arg Leu Val Thr Gly Gln Arg Cys Asp Gln Cys Leu Pro Gln
                485                 490                 495

His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys
            500                 505                 510

Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Ser Glu Asp Ser Gly Gln
        515                 520                 525

Cys Ser Cys Leu Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu
    530                 535                 540

Ser Gly Tyr Tyr Phe Thr Thr Leu Asp His Tyr Ile Tyr Glu Ala Glu
545                 550                 555                 560

Glu Ala Asn Leu Gly Pro Gly Val Val Val Val Glu Arg Gln Tyr Ile
                565                 570                 575

Gln Asp Arg Ile Pro Ser Trp Thr Gly Pro Gly Phe Val Arg Val Pro
            580                 585                 590

Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met
        595                 600                 605

Glu Tyr Glu Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp
    610                 615                 620

Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Lys Ile Pro Ala Ser
625                 630                 635                 640

Ser Arg Cys Gly Asn Thr Val Pro Asp Asp Asp Asn Gln Val Val Ser
                645                 650                 655

Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe
            660                 665                 670

Glu Lys Gly Met Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr
        675                 680                 685

Ala Ser Gly Ser Asp Val Glu Ser Pro Tyr Thr Phe Ile Asp Ser Leu
    690                 695                 700
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Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly
705                 710                 715                 720

Ser Gly Asp Gly Glu Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg
                725                 730                 735

Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr
            740                 745                 750

Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Ile His Gln
        755                 760                 765

Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val
    770                 775                 780

Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly
785                 790                 795                 800

Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Asn
                805                 810                 815

Gly Cys Lys Pro Cys Asp Cys His Leu Gln Gly Ser Ala Ser Ala Phe
            820                 825                 830

Cys Asp Ala Ile Thr Gly Gln Cys His Cys Phe Gln Gly Ile Tyr Ala
        835                 840                 845

Arg Gln Cys Asp Arg Cys Leu Pro Gly Tyr Trp Gly Phe Pro Ser Cys
    850                 855                 860

Gln Pro Cys Gln Cys Asn Gly His Ala Leu Asp Cys Asp Thr Val Thr
865                 870                 875                 880

Gly Glu Cys Leu Ser Cys Gln Asp Tyr Thr Thr Gly His Asn Cys Glu
                885                 890                 895

Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly Ser Gly Asp
            900                 905                 910

His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser Gly Arg Gln
        915                 920                 925

Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln Leu Ala Cys
    930                 935                 940

Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp Cys Ala Ser
945                 950                 955                 960

Gly Phe Phe Gly Asn Pro Ser Asp Phe Gly Gly Ser Cys Gln Pro Cys
                965                 970                 975

Gln Cys His His Asn Ile Asp Thr Thr Asp Pro Glu Ala Cys Asp Lys
            980                 985                 990

Asp Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Asp His
        995                1000                1005

Cys Gln Leu Cys Gln Tyr Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp
   1010                1015                1020
```

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Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Lys Glu His Cys
1025               1030                1035                1040

Asn Gly Ser Asp Cys His Cys Asp Lys Ala Thr Gly Gln Cys Ser Cys
                1045                1050                1055

Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr
            1060                1065                1070

Trp Gln Leu Ala Ser Gly Thr Gly Cys Gly Pro Cys Asn Cys Asn Ala
        1075                1080                1085

Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln
    1090                1095                1100

Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu
1105                1110                1115                1120

Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro
                1125                1130                1135

Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val
            1140                1145                1150

Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly
        1155                1160                1165

Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala
    1170                1175                1180

Leu Trp Asp Ala Ile Ile Gly Glu Leu Thr Asn Arg Thr His Lys Phe
1185                1190                1195                1200

Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr
                1205                1210                1215

Arg Glu Thr Val Asp Ser Val Glu Lys Lys Val Asn Glu Ile Lys Asp
            1220                1225                1230

Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Ile
        1235                1240                1245

Leu Phe Glu Glu Ala Glu Lys Leu Thr Lys Asp Val Thr Glu Lys Met
    1250                1255                1260

Ala Gln Val Glu Val Lys Leu Thr Asp Thr Ala Ser Gln Ser Asn Ser
1265                1270                1275                1280

Thr Ala Gly Glu Leu Gly Ala Leu Gln Ala Glu Ala Glu Ser Leu Asp
                1285                1290                1295

Lys Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser
            1300                1305                1310

Asp Ile Gln Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser
        1315                1320                1325

Leu Glu Ala Glu Lys Arg Val Asn Ala Ser Thr Thr Asp Pro Asn Ser
    1330                1335                1340

Thr Val Glu Gln Ser Ala Leu Thr Arg Asp Arg Val Glu Asp Leu Met
```

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1345                1350                1355                1360

Leu Glu Arg Glu Ser Pro Phe Lys Glu Gln Gln Glu Glu Gln Ala Arg
                  1365                1370                1375

Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala
            1380                1385                1390

Ala Ala Gln Met Thr Cys Gly Thr Pro Pro Gly Ala Asp Cys Ser Glu
        1395                1400                1405

Ser Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Lys Lys
    1410                1415                1420

Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Ser Ala
1425                1430                1435                1440

Trp Gln Lys Ala Met Asp Phe Asp Arg Asp Val Leu Ser Ala Leu Ala
                  1445                1450                1455

Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Val Arg Ala
            1460                1465                1470

Asp Glu Ala Lys Gln Asn Ala Gln Asp Val Leu Leu Lys Thr Asn Ala
        1475                1480                1485

Thr Lys Glu Lys Val Asp Lys Ser Asn Glu Asp Leu Arg Asn Leu Ile
    1490                1495                1500

Lys Gln Ile Arg Asn Phe Leu Thr Glu Asp Ser Ala Asp Leu Asp Ser
1505                1510                1515                1520

Ile Glu Ala Val Ala Asn Glu Val Leu Lys Ser Gly Asn Ala Ser Thr
                  1525                1530                1535

Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu
            1540                1545                1550

Thr Leu Ser Gln Val Glu Val Ile Leu Gln Gln Ser Ala Ala Asp Ile
        1555                1560                1565

Ala Arg Ala Glu Leu Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser
    1570                1575                1580

Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu
1585                1590                1595                1600

Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala
                  1605                1610                1615

Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser
            1620                1625                1630

Glu Thr Ala Ala Ser Glu Glu Thr Leu Thr Asn Ala Ser Gln Arg Ile
        1635                1640                1645

Ser Lys Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln
    1650                1655                1660

Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Ser Val Lys
1665                1670                1675                1680
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Gln Asn Ala Asp Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu
                1685                1690                1695

Lys Tyr Lys Lys Val Glu Ser Leu Ile Ala Gln Lys Thr Glu Glu Ser
            1700                1705                1710

Ala Asp Ala Arg Arg Lys Ala Glu Leu Leu Gln Asn Glu Ala Lys Thr
        1715                1720                1725

Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Glu Asp Leu Glu
    1730                1735                1740

Arg Lys Tyr Glu Asp Asn Gln Lys Tyr Leu Glu Asp Lys Ala Gln Glu
1745                1750                1755                1760

Leu Val Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser
                1765                1770                1775

Glu Lys Val Ala Val Tyr Ser Thr Cys Leu
            1780                1785


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Glu Pro Tyr Cys Ile Val Ser His Leu Gln Glu Asp Lys Lys Cys Phe
  1               5                  10                  15

ata tgt gac tcc cga gac cct tat cac gag acc ctc aac ccc gac agc   96
Ile Cys Asp Ser Arg Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser
             20                  25                  30

cat ctc att gag aac gtg gtc acc aca ttt gct cca aac cgc ctt aag   144
His Leu Ile Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys
         35                  40                  45

atc tgg tgg caa tcg gaa aat ggt gtg gag aac gtg acc atc caa ctg   192
Ile Trp Trp Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu
     50                  55                  60

gac ctg gaa gca gaa ttc cat ttc act cat ctc atc atg acc ttc aag   240
Asp Leu Glu Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys
 65                  70                  75                  80

aca ttc cgc cca gcc gcc atg ctg atc gag cgg tct tct gac ttt ggg   288
Thr Phe Arg Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly
                 85                  90                  95

aag act tgg ggc gtg tac aga tac ttc gcc tac gac tgt gag agc tcg   336
Lys Thr Trp Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ser Ser
            100                 105                 110
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ttc cca ggc att tca act gga ccc atg aag aaa gtg gat gac atc atc   384
Phe Pro Gly Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile
        115                 120                 125

tgt gac tct cga tat tct gac att gag ccc tcg aca gaa gga gag gta   432
Cys Asp Ser Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val
    130                 135                 140

ata ttt cgt gct tta gat cct gct ttc aaa att gaa gac cct tat agt   480
Ile Phe Arg Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser
145                 150                 155                 160

cca agg ata cag aat cta tta aaa atc acc aac ttg aga atc aag ttt   528
Pro Arg Ile Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe
                165                 170                 175

gtg aaa ctg cac acc ttg ggg gat aac ctt ttg gac tcc aga atg gaa   576
Val Lys Leu His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu
            180                 185                 190

atc cga gag aag tac tat tac gct gtt tat gat atg gtg gtt cga ggg   624
Ile Arg Glu Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly
        195                 200                 205

aac tgc ttc tgc tat ggc cac gcc agt gaa tgc gcc cct gtg gat gga   672
Asn Cys Phe Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly
    210                 215                 220

gtc aat gaa gaa gtg gaa gga atg gtt cac ggg cac tgc atg tgc aga   720
Val Asn Glu Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg
225                 230                 235                 240

cac aac acc aaa ggc ctg aac tgt gag ctg tgc atg gat ttc tac cac   768
His Asn Thr Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His
                245                 250                 255

gat ttg ccg tgg aga cct gct gaa ggc cgg aac agc aac gcc tgc aaa   816
Asp Leu Pro Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys
            260                 265                 270

aaa tgt aac tgc aat gaa cat tcc agc tcg tgt cac ttt gac atg gca   864
Lys Cys Asn Cys Asn Glu His Ser Ser Ser Cys His Phe Asp Met Ala
        275                 280                 285

gtc ttc ctg gct act ggc aac gtc agc ggg gga gtg tgt gat aac tgt   912
Val Phe Leu Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asn Cys
    290                 295                 300

cag cac aac acc atg ggg cgc aac tgt gaa cag tgc aaa ccg ttc tac   960
Gln His Asn Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr
305                 310                 315                 320

ttc cag cac cct gag agg gac atc cgg gac ccc aat ctc tgt gaa cca  1008
Phe Gln His Pro Glu Arg Asp Ile Arg Asp Pro Asn Leu Cys Glu Pro
                325                 330                 335

tgt acc tgt gac cca gct ggt tct gag aat ggc ggg atc tgt gat ggg  1056
Cys Thr Cys Asp Pro Ala Gly Ser Glu Asn Gly Gly Ile Cys Asp Gly
            340                 345                 350

tac act gat ttt tct gtg ggt ctc att gct ggt cag tgt cgg tgc aaa  1104
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Tyr Thr Asp Phe Ser Val Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys
        355                 360                 365

ttg cac gtg gag gga gag cgc tgt gat gtt tgt aaa gaa ggc ttc tac   1152
Leu His Val Glu Gly Glu Arg Cys Asp Val Cys Lys Glu Gly Phe Tyr
    370                 375                 380

gac tta agt gct gaa gac ccg tat ggt tgt aaa tca tgt gct tgc aat   1200
Asp Leu Ser Ala Glu Asp Pro Tyr Gly Cys Lys Ser Cys Ala Cys Asn
385                 390                 395                 400

cct ctg gga aca att cct ggt ggg aat cct tgt gat tct gag act ggc   1248
Pro Leu Gly Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly
                405                 410                 415

tac tgc tac tgt aag cgc ctg gtg aca gga cag cgc tgt gac cag tgc   1296
Tyr Cys Tyr Cys Lys Arg Leu Val Thr Gly Gln Arg Cys Asp Gln Cys
            420                 425                 430

ctg ccg cag cac tgg ggt tta agc aat gat ttg gat ggg tgt cga cct   1344
Leu Pro Gln His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro
        435                 440                 445

tgt gac tgt gac ctt gga ggg gcg ctg aac aat agc tgc tcc gag gac   1392
Cys Asp Cys Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Ser Glu Asp
    450                 455                 460

tcc ggc cag tgc tcc tgc ctg ccc cac atg att ggg cgg cag tgt aac   1440
Ser Gly Gln Cys Ser Cys Leu Pro His Met Ile Gly Arg Gln Cys Asn
465                 470                 475                 480

gag gtg gag tcc ggt tac tac ttc acc acc ctg gac cac tac atc tac   1488
Glu Val Glu Ser Gly Tyr Tyr Phe Thr Thr Leu Asp His Tyr Ile Tyr
                485                 490                 495

gaa gcc gag gaa gcc aat ctg ggg cct gga gtc gtt gtg gtg gaa agg   1536
Glu Ala Glu Glu Ala Asn Leu Gly Pro Gly Val Val Val Val Glu Arg
            500                 505                 510

cag tac att cag gac cgc att cct tcc tgg aca gga cct ggc ttc gtc   1584
Gln Tyr Ile Gln Asp Arg Ile Pro Ser Trp Thr Gly Pro Gly Phe Val
        515                 520                 525

cgg gtg cct gaa ggg gct tat ttg gag ttt ttc att gac aac ata cca   1632
Arg Val Pro Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro
    530                 535                 540

tat tcc atg gag tat gaa atc ctg att cgc tat gag cca cag ctg ccg   1680
Tyr Ser Met Glu Tyr Glu Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro
545                 550                 555                 560

gac cac tgg gag aaa gct gtc atc act gta cag cgg ccg ggg aag att   1728
Asp His Trp Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Lys Ile
                565                 570                 575

cca gcc agc agc cga tgt ggt aac acc gtt ccc gat gat gac aac cag   1776
Pro Ala Ser Ser Arg Cys Gly Asn Thr Val Pro Asp Asp Asp Asn Gln
            580                 585                 590

gtg gtg tcc ttg tca ccg ggc tca aga tac gtt gtc ctc cct cgc ccc   1824
Val Val Ser Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro
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        595                 600                 605

gtg tgc ttt gag aag gga atg aac tac acg gtg agg ttg gag ctg ccc   1872
Val Cys Phe Glu Lys Gly Met Asn Tyr Thr Val Arg Leu Glu Leu Pro
    610                 615                 620

cag tat acg gca tcg ggc agt gac gtg gag agc cct tac acg ttc atc   1920
Gln Tyr Thr Ala Ser Gly Ser Asp Val Glu Ser Pro Tyr Thr Phe Ile
625                 630                 635                 640

gac tcg ctt gtt ctc atg ccc tac tgt aaa tcg ctg gac atc ttc act   1968
Asp Ser Leu Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr
                645                 650                 655

gtt ggc ggc tca ggc gat ggg gag gtc acc aat agt gcc tgg gaa acc   2016
Val Gly Gly Ser Gly Asp Gly Glu Val Thr Asn Ser Ala Trp Glu Thr
            660                 665                 670

ttc cag cgc tac agg tgt ctg gag aac agc agg agt gtg gta aaa aca   2064
Phe Gln Arg Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr
        675                 680                 685

ccc atg aca gat gtc tgc aga aac att atc ttc agc att tct gcc ttg   2112
Pro Met Thr Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu
    690                 695                 700

att cac cag acg ggc ctt gct tgt gaa tgt gac ccc cag gga tct ctg   2160
Ile His Gln Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu
705                 710                 715                 720

agt tct gtg tgt gac ccc aat ggt ggc cag tgc cag tgc cgt cct aat   2208
Ser Ser Val Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn
                725                 730                 735

gtg gtt gga aga acc tgc aac agg tgt gcc ccg ggc acc ttt ggc ttt   2256
Val Val Gly Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe
            740                 745                 750

ggc ccc aac gga tgc aaa cct tgt gac tgc cat ctg caa ggg tct gcc   2304
Gly Pro Asn Gly Cys Lys Pro Cys Asp Cys His Leu Gln Gly Ser Ala
        755                 760                 765

agt gcc ttc tgc gat gcg atc act ggc cag tgc cac tgt ttc cag ggc   2352
Ser Ala Phe Cys Asp Ala Ile Thr Gly Gln Cys His Cys Phe Gln Gly
    770                 775                 780

atc tat gct cgg cag tgt gac cga tgt ctc cct ggg tat tgg ggc ttt   2400
Ile Tyr Ala Arg Gln Cys Asp Arg Cys Leu Pro Gly Tyr Trp Gly Phe
785                 790                 795                 800

ccc agc tgc cag ccc tgc cag tgt aat ggt cat gct cta gac tgt gac   2448
Pro Ser Cys Gln Pro Cys Gln Cys Asn Gly His Ala Leu Asp Cys Asp
                805                 810                 815

aca gtg aca ggg gag tgt ctg agc tgt cag gac tac acc acg ggc cac   2496
Thr Val Thr Gly Glu Cys Leu Ser Cys Gln Asp Tyr Thr Thr Gly His
            820                 825                 830

aac tgc gaa agg tgc ctg gct ggc tac tac ggt gat ccc atc att ggg   2544
Asn Cys Glu Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly
        835                 840                 845
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tca gga gac cac tgt cgc cct tgc cct tgt cct gat ggt cct gac agt   2592
Ser Gly Asp His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser
    850                 855                 860

gga cga cag ttt gcc agg agc tgt tat caa gac ccc gtc act ctc cag   2640
Gly Arg Gln Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln
865                 870                 875                 880

ctt gcg tgt gtt tgt gat cct ggg tac att ggc tcc aga tgt gat gac   2688
Leu Ala Cys Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp
                885                 890                 895

tgt gcc tct gga ttt ttt ggc aat ccc tca gac ttt ggg ggt tca tgt   2736
Cys Ala Ser Gly Phe Phe Gly Asn Pro Ser Asp Phe Gly Gly Ser Cys
            900                 905                 910

caa ccg tgt cag tgc cac cac aac att gac act acc gat cca gaa gcc   2784
Gln Pro Cys Gln Cys His His Asn Ile Asp Thr Thr Asp Pro Glu Ala
        915                 920                 925

tgt gac aag gac acg gga cga tgc ctc aag tgc ctg tac cac acg gaa   2832
Cys Asp Lys Asp Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu
    930                 935                 940

ggg gac cat tgc cag ctc tgc cag tat ggg tac tac ggc gat gct ctt   2880
Gly Asp His Cys Gln Leu Cys Gln Tyr Gly Tyr Tyr Gly Asp Ala Leu
945                 950                 955                 960

cgg caa gac tgt aga aag tgt gtc tgc aat tac ctg ggc acg gtg aag   2928
Arg Gln Asp Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Lys
                965                 970                 975

gaa cat tgt aat ggc tct gac tgc cac tgt gac aaa gcc act ggt cag   2976
Glu His Cys Asn Gly Ser Asp Cys His Cys Asp Lys Ala Thr Gly Gln
            980                 985                 990

tgc tcg tgc ctt ccc aat gtg atc ggg cag aac tgt gac cgg tgt gcg   3024
Cys Ser Cys Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala
        995                1000                1005

ccc aac acc tgg cag ctg gct agc ggg act ggc tgc ggg ccc tgc aat   3072
Pro Asn Thr Trp Gln Leu Ala Ser Gly Thr Gly Cys Gly Pro Cys Asn
   1010                1015                1020

tgc aat gct gcg cat tcc ttt ggg cca tcc tgc aac gag ttc aca ggg   3120
Cys Asn Ala Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly
1025                1030                1035                1040

cag tgc cag tgc atg ccg ggc ttt gga ggc cga acc tgc agc gag tgc   3168
Gln Cys Gln Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys
                1045                1050                1055

cag gag ctc ttc tgg gga gac cct gat gtg gaa tgc cga gcc tgt gac   3216
Gln Glu Leu Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp
            1060                1065                1070

tgt gat ccc agg ggc att gag aca cct cag tgt gac cag tcc acg ggc   3264
Cys Asp Pro Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly
        1075                1080                1085
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cag tgt gtc tgt gtg gag ggt gta gag ggt cct cgc tgc gac aag tgc   3312
Gln Cys Val Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys
   1090                1095                1100

acc aga ggt tac tcg ggg gtc ttt cct gac tgc aca ccc tgc cac cag   3360
Thr Arg Gly Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln
1105                1110                1115                1120

tgc ttt gct ctc tgg gat gct atc att ggt gag ctg acc aac agg acc   3408
Cys Phe Ala Leu Trp Asp Ala Ile Ile Gly Glu Leu Thr Asn Arg Thr
                1125                1130                1135

cac aaa ttc ctg gag aaa gcc aag gct ctg aaa atc agt ggt gtg att   3456
His Lys Phe Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile
            1140                1145                1150

ggt ccc tac cga gag acc gtg gac tct gta gag aag aaa gtc aat gag   3504
Gly Pro Tyr Arg Glu Thr Val Asp Ser Val Glu Lys Lys Val Asn Glu
        1155                1160                1165

ata aaa gac atc ctg gcc cag agc cca gca gcg gaa cca ctg aaa aac   3552
Ile Lys Asp Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn
    1170                1175                1180

att ggc att ctc ttc gag gag gca gag aaa cta acc aaa gat gtc aca   3600
Ile Gly Ile Leu Phe Glu Glu Ala Glu Lys Leu Thr Lys Asp Val Thr
1185                1190                1195                1200

gaa aag atg gcg cag gta gaa gtg aaa tta act gat aca gct tca cag   3648
Glu Lys Met Ala Gln Val Glu Val Lys Leu Thr Asp Thr Ala Ser Gln
                1205                1210                1215

agt aac agc aca gct gga gag ctc ggc gca ctg cag gca gaa gca gag   3696
Ser Asn Ser Thr Ala Gly Glu Leu Gly Ala Leu Gln Ala Glu Ala Glu
            1220                1225                1230

agc ctt gac aag acc gtg aag gag ctg gca gaa cag ctg gag ttt atc   3744
Ser Leu Asp Lys Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile
        1235                1240                1245

aaa aac tcc gat att cag ggc gcc ttg gat agc atc acc aag tat ttc   3792
Lys Asn Ser Asp Ile Gln Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe
    1250                1255                1260

cag atg tct ctt gag gca gag aag cgg gtg aat gcc tcc acc aca gac   3840
Gln Met Ser Leu Glu Ala Glu Lys Arg Val Asn Ala Ser Thr Thr Asp
1265                1270                1275                1280

ccc aac agc act gtg gag cag tct gcc ctc acg cga gac aga gta gaa   3888
Pro Asn Ser Thr Val Glu Gln Ser Ala Leu Thr Arg Asp Arg Val Glu
                1285                1290                1295

gat ctg atg ttg gag cga gag tct ccg ttc aag gag cag cag gag gaa   3936
Asp Leu Met Leu Glu Arg Glu Ser Pro Phe Lys Glu Gln Gln Glu Glu
            1300                1305                1310

cag gca cgc ctc ctg gac gaa ctg gcc ggc aaa ctg caa agt ctc gac   3984
Gln Ala Arg Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp
        1315                1320                1325

ctg tcg gct gct gca cag atg acc tgt gga aca cct cca ggg gct gac   4032
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Leu Ser Ala Ala Ala Gln Met Thr Cys Gly Thr Pro Pro Gly Ala Asp
   1330                1335                1340

tgt tct gaa agt gaa tgt ggt ggc ccc aac tgc aga act gac gaa gga   4080
Cys Ser Glu Ser Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly
1345                1350                1355                1360

gag aag aag tgt ggg ggg cct ggc tgt ggt ggt ctg gtc act gtg gcc   4128
Glu Lys Lys Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala
               1365                1370                1375

cac agt gct tgg cag aaa gcc atg gat ttt gac cgt gat gtc ctg agt   4176
His Ser Ala Trp Gln Lys Ala Met Asp Phe Asp Arg Asp Val Leu Ser
           1380                1385                1390

gcc ctg gct gaa gtc gaa cag ctc tcc aag atg gtc tct gaa gca aaa   4224
Ala Leu Ala Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys
       1395                1400                1405

gtg aga gca gat gag gcg aag cag aat gcg cag gat gtc ctg tta aaa   4272
Val Arg Ala Asp Glu Ala Lys Gln Asn Ala Gln Asp Val Leu Leu Lys
   1410                1415                1420

aca aat gct acc aaa gaa aaa gtg gac aag agc aac gag gac ctg cgg   4320
Thr Asn Ala Thr Lys Glu Lys Val Asp Lys Ser Asn Glu Asp Leu Arg
1425                1430                1435                1440

aac ctc atc aag cag atc aga aac ttc ctg act gag gat agt gct gat   4368
Asn Leu Ile Lys Gln Ile Arg Asn Phe Leu Thr Glu Asp Ser Ala Asp
               1445                1450                1455

cta gac agt att gaa gca gtt gct aat gaa gta ctg aaa agt gga aat   4416
Leu Asp Ser Ile Glu Ala Val Ala Asn Glu Val Leu Lys Ser Gly Asn
           1460                1465                1470

gct agc acg cca cag cag tta cag aac cta aca gaa gac att cgg gag   4464
Ala Ser Thr Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu
       1475                1480                1485

cga gtt gaa acc ctc tct caa gta gag gtt att ttg cag cag agt gca   4512
Arg Val Glu Thr Leu Ser Gln Val Glu Val Ile Leu Gln Gln Ser Ala
   1490                1495                1500

gct gac att gcc aga gct gag ctg ttg ctt gag gaa gct aag aga gca   4560
Ala Asp Ile Ala Arg Ala Glu Leu Leu Leu Glu Glu Ala Lys Arg Ala
1505                1510                1515                1520

agc aaa agt gca aca gat gtt aaa gtc act gca gac atg gtg aag gaa   4608
Ser Lys Ser Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu
               1525                1530                1535

gca tta gaa gaa gca gaa aag gcc cag gtt gca gca gag aag gcg att   4656
Ala Leu Glu Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile
           1540                1545                1550

aaa caa gct gat gag gat atc caa gga acc caa aac ctg cta aca tcg   4704
Lys Gln Ala Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser
       1555                1560                1565

att gaa tct gaa acg gca gct tct gag gaa acc ctg acc aac gcc tcc   4752
Ile Glu Ser Glu Thr Ala Ala Ser Glu Glu Thr Leu Thr Asn Ala Ser
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   1570                1575                1580

cag cgc atc agc aag ctt gag agg aac gtg gaa gag ctt aag cgt aaa   4800
Gln Arg Ile Ser Lys Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys
1585                1590                1595                1600

gct gcc cag aac tct ggg gag gca gaa tat atc gaa aaa gta gta tat   4848
Ala Ala Gln Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr
                1605                1610                1615

tct gta aaa cag aat gca gac gat gtt aaa aag act cta gat ggc gaa   4896
Ser Val Lys Gln Asn Ala Asp Asp Val Lys Lys Thr Leu Asp Gly Glu
            1620                1625                1630

ctt gat gaa aag tat aag aag gta gaa agt tta att gcc caa aaa act   4944
Leu Asp Glu Lys Tyr Lys Lys Val Glu Ser Leu Ile Ala Gln Lys Thr
        1635                1640                1645

gaa gag tca gca gat gcc agg agg aaa gct gag ctg cta caa aat gaa   4992
Glu Glu Ser Ala Asp Ala Arg Arg Lys Ala Glu Leu Leu Gln Asn Glu
    1650                1655                1660

gca aaa aca ctc ttg gct caa gct aac agc aag ctc cag ctg ttg gaa   5040
Ala Lys Thr Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Glu
1665                1670                1675                1680

gac tta gaa aga aaa tat gag gac aat caa aaa tac tta gaa gat aaa   5088
Asp Leu Glu Arg Lys Tyr Glu Asp Asn Gln Lys Tyr Leu Glu Asp Lys
                1685                1690                1695

gct caa gaa ttg gtg cga ctg gaa gga gag gtt cgc tcc ctc ctt aag   5136
Ala Gln Glu Leu Val Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys
            1700                1705                1710

gac ata agt gag aaa gtt gcg gtt tac agc acc tgc tta taacaggaag    5185
Asp Ile Ser Glu Lys Val Ala Val Tyr Ser Thr Cys Leu
        1715                1720                1725

gggctgtaga ggggctcggt gaccaaggta aaccacacgc gcaaaccgag gcagtcatct 5245

acaaataacc catcatctat ttaatgtttt taaccaccta cttttgtatg gagttaaata 5305

aaagacattg gttttgtata aaca                                        5329


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Ile Cys Asp Ser Arg Asp Pro Tyr His Glu Thr Leu Asn Pro Asp Ser
             20                  25                  30

His Leu Ile Glu Asn Val Val Thr Thr Phe Ala Pro Asn Arg Leu Lys
         35                  40                  45

Ile Trp Trp Gln Ser Glu Asn Gly Val Glu Asn Val Thr Ile Gln Leu
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     50                  55                  60

Asp Leu Glu Ala Glu Phe His Phe Thr His Leu Ile Met Thr Phe Lys
 65                  70                  75                  80

Thr Phe Arg Pro Ala Ala Met Leu Ile Glu Arg Ser Ser Asp Phe Gly
                 85                  90                  95

Lys Thr Trp Gly Val Tyr Arg Tyr Phe Ala Tyr Asp Cys Glu Ser Ser
            100                 105                 110

Phe Pro Gly Ile Ser Thr Gly Pro Met Lys Lys Val Asp Asp Ile Ile
        115                 120                 125

Cys Asp Ser Arg Tyr Ser Asp Ile Glu Pro Ser Thr Glu Gly Glu Val
    130                 135                 140

Ile Phe Arg Ala Leu Asp Pro Ala Phe Lys Ile Glu Asp Pro Tyr Ser
145                 150                 155                 160

Pro Arg Ile Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe
                165                 170                 175

Val Lys Leu His Thr Leu Gly Asp Asn Leu Leu Asp Ser Arg Met Glu
            180                 185                 190

Ile Arg Glu Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly
        195                 200                 205

Asn Cys Phe Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly
    210                 215                 220

Val Asn Glu Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg
225                 230                 235                 240

His Asn Thr Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His
                245                 250                 255

Asp Leu Pro Trp Arg Pro Ala Glu Gly Arg Asn Ser Asn Ala Cys Lys
            260                 265                 270

Lys Cys Asn Cys Asn Glu His Ser Ser Ser Cys His Phe Asp Met Ala
        275                 280                 285

Val Phe Leu Ala Thr Gly Asn Val Ser Gly Gly Val Cys Asp Asn Cys
    290                 295                 300

Gln His Asn Thr Met Gly Arg Asn Cys Glu Gln Cys Lys Pro Phe Tyr
305                 310                 315                 320

Phe Gln His Pro Glu Arg Asp Ile Arg Asp Pro Asn Leu Cys Glu Pro
                325                 330                 335

Cys Thr Cys Asp Pro Ala Gly Ser Glu Asn Gly Gly Ile Cys Asp Gly
            340                 345                 350

Tyr Thr Asp Phe Ser Val Gly Leu Ile Ala Gly Gln Cys Arg Cys Lys
        355                 360                 365

Leu His Val Glu Gly Glu Arg Cys Asp Val Cys Lys Glu Gly Phe Tyr
    370                 375                 380
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Asp Leu Ser Ala Glu Asp Pro Tyr Gly Cys Lys Ser Cys Ala Cys Asn
385                 390                 395                 400

Pro Leu Gly Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly
                405                 410                 415

Tyr Cys Tyr Cys Lys Arg Leu Val Thr Gly Gln Arg Cys Asp Gln Cys
            420                 425                 430

Leu Pro Gln His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro
        435                 440                 445

Cys Asp Cys Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Ser Glu Asp
    450                 455                 460

Ser Gly Gln Cys Ser Cys Leu Pro His Met Ile Gly Arg Gln Cys Asn
465                 470                 475                 480

Glu Val Glu Ser Gly Tyr Tyr Phe Thr Thr Leu Asp His Tyr Ile Tyr
                485                 490                 495

Glu Ala Glu Glu Ala Asn Leu Gly Pro Gly Val Val Val Val Glu Arg
            500                 505                 510

Gln Tyr Ile Gln Asp Arg Ile Pro Ser Trp Thr Gly Pro Gly Phe Val
        515                 520                 525

Arg Val Pro Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro
    530                 535                 540

Tyr Ser Met Glu Tyr Glu Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro
545                 550                 555                 560

Asp His Trp Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Lys Ile
                565                 570                 575

Pro Ala Ser Ser Arg Cys Gly Asn Thr Val Pro Asp Asp Asp Asn Gln
            580                 585                 590

Val Val Ser Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro
        595                 600                 605

Val Cys Phe Glu Lys Gly Met Asn Tyr Thr Val Arg Leu Glu Leu Pro
    610                 615                 620

Gln Tyr Thr Ala Ser Gly Ser Asp Val Glu Ser Pro Tyr Thr Phe Ile
625                 630                 635                 640

Asp Ser Leu Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr
                645                 650                 655

Val Gly Gly Ser Gly Asp Gly Glu Val Thr Asn Ser Ala Trp Glu Thr
            660                 665                 670

Phe Gln Arg Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr
        675                 680                 685

Pro Met Thr Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu
    690                 695                 700
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Ile His Gln Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu
705                 710                 715                 720

Ser Ser Val Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn
                725                 730                 735

Val Val Gly Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe
            740                 745                 750

Gly Pro Asn Gly Cys Lys Pro Cys Asp Cys His Leu Gln Gly Ser Ala
        755                 760                 765

Ser Ala Phe Cys Asp Ala Ile Thr Gly Gln Cys His Cys Phe Gln Gly
    770                 775                 780

Ile Tyr Ala Arg Gln Cys Asp Arg Cys Leu Pro Gly Tyr Trp Gly Phe
785                 790                 795                 800

Pro Ser Cys Gln Pro Cys Gln Cys Asn Gly His Ala Leu Asp Cys Asp
                805                 810                 815

Thr Val Thr Gly Glu Cys Leu Ser Cys Gln Asp Tyr Thr Thr Gly His
            820                 825                 830

Asn Cys Glu Arg Cys Leu Ala Gly Tyr Tyr Gly Asp Pro Ile Ile Gly
        835                 840                 845

Ser Gly Asp His Cys Arg Pro Cys Pro Cys Pro Asp Gly Pro Asp Ser
    850                 855                 860

Gly Arg Gln Phe Ala Arg Ser Cys Tyr Gln Asp Pro Val Thr Leu Gln
865                 870                 875                 880

Leu Ala Cys Val Cys Asp Pro Gly Tyr Ile Gly Ser Arg Cys Asp Asp
                885                 890                 895

Cys Ala Ser Gly Phe Phe Gly Asn Pro Ser Asp Phe Gly Gly Ser Cys
            900                 905                 910

Gln Pro Cys Gln Cys His His Asn Ile Asp Thr Thr Asp Pro Glu Ala
        915                 920                 925

Cys Asp Lys Asp Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu
    930                 935                 940

Gly Asp His Cys Gln Leu Cys Gln Tyr Gly Tyr Tyr Gly Asp Ala Leu
945                 950                 955                 960

Arg Gln Asp Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Lys
                965                 970                 975

Glu His Cys Asn Gly Ser Asp Cys His Cys Asp Lys Ala Thr Gly Gln
            980                 985                 990

Cys Ser Cys Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala
        995                1000                1005

Pro Asn Thr Trp Gln Leu Ala Ser Gly Thr Gly Cys Gly Pro Cys Asn
   1010                1015                1020

Cys Asn Ala Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly
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1025                1030                1035                1040

Gln Cys Gln Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys
                1045                1050                1055

Gln Glu Leu Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp
            1060                1065                1070

Cys Asp Pro Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly
        1075                1080                1085

Gln Cys Val Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys
    1090                1095                1100

Thr Arg Gly Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln
1105                1110                1115                1120

Cys Phe Ala Leu Trp Asp Ala Ile Ile Gly Glu Leu Thr Asn Arg Thr
                1125                1130                1135

His Lys Phe Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile
            1140                1145                1150

Gly Pro Tyr Arg Glu Thr Val Asp Ser Val Glu Lys Lys Val Asn Glu
        1155                1160                1165

Ile Lys Asp Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn
    1170                1175                1180

Ile Gly Ile Leu Phe Glu Glu Ala Glu Lys Leu Thr Lys Asp Val Thr
1185                1190                1195                1200

Glu Lys Met Ala Gln Val Glu Val Lys Leu Thr Asp Thr Ala Ser Gln
                1205                1210                1215

Ser Asn Ser Thr Ala Gly Glu Leu Gly Ala Leu Gln Ala Glu Ala Glu
            1220                1225                1230

Ser Leu Asp Lys Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile
        1235                1240                1245

Lys Asn Ser Asp Ile Gln Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe
    1250                1255                1260

Gln Met Ser Leu Glu Ala Glu Lys Arg Val Asn Ala Ser Thr Thr Asp
1265                1270                1275                1280

Pro Asn Ser Thr Val Glu Gln Ser Ala Leu Thr Arg Asp Arg Val Glu
                1285                1290                1295

Asp Leu Met Leu Glu Arg Glu Ser Pro Phe Lys Glu Gln Gln Glu Glu
            1300                1305                1310

Gln Ala Arg Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp
        1315                1320                1325

Leu Ser Ala Ala Ala Gln Met Thr Cys Gly Thr Pro Pro Gly Ala Asp
    1330                1335                1340

Cys Ser Glu Ser Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly
1345                1350                1355                1360
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Glu Lys Lys Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala
                1365                1370                1375

His Ser Ala Trp Gln Lys Ala Met Asp Phe Asp Arg Asp Val Leu Ser
            1380                1385                1390

Ala Leu Ala Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys
        1395                1400                1405

Val Arg Ala Asp Glu Ala Lys Gln Asn Ala Gln Asp Val Leu Leu Lys
    1410                1415                1420

Thr Asn Ala Thr Lys Glu Lys Val Asp Lys Ser Asn Glu Asp Leu Arg
1425                1430                1435                1440

Asn Leu Ile Lys Gln Ile Arg Asn Phe Leu Thr Glu Asp Ser Ala Asp
                1445                1450                1455

Leu Asp Ser Ile Glu Ala Val Ala Asn Glu Val Leu Lys Ser Gly Asn
            1460                1465                1470

Ala Ser Thr Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu
        1475                1480                1485

Arg Val Glu Thr Leu Ser Gln Val Glu Val Ile Leu Gln Gln Ser Ala
    1490                1495                1500

Ala Asp Ile Ala Arg Ala Glu Leu Leu Leu Glu Glu Ala Lys Arg Ala
1505                1510                1515                1520

Ser Lys Ser Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu
                1525                1530                1535

Ala Leu Glu Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile
            1540                1545                1550

Lys Gln Ala Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser
        1555                1560                1565

Ile Glu Ser Glu Thr Ala Ala Ser Glu Glu Thr Leu Thr Asn Ala Ser
    1570                1575                1580

Gln Arg Ile Ser Lys Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys
1585                1590                1595                1600

Ala Ala Gln Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr
                1605                1610                1615

Ser Val Lys Gln Asn Ala Asp Asp Val Lys Lys Thr Leu Asp Gly Glu
            1620                1625                1630

Leu Asp Glu Lys Tyr Lys Lys Val Glu Ser Leu Ile Ala Gln Lys Thr
        1635                1640                1645

Glu Glu Ser Ala Asp Ala Arg Arg Lys Ala Glu Leu Leu Gln Asn Glu
    1650                1655                1660

Ala Lys Thr Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Glu
1665                1670                1675                1680
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Asp Leu Glu Arg Lys Tyr Glu Asp Asn Gln Lys Tyr Leu Glu Asp Lys
                1685                1690                1695

Ala Gln Glu Leu Val Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys
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Asp Ile Ser Glu Lys Val Ala Val Tyr Ser Thr Cys Leu
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cgccgccacc gcccgcgccg gagtcaggcc cctgggcccc caggctcaag cagcgaagcg 180

gcctccgggg gacgccgcta ggcgagagga acgcgccggt gcccttgcct tcgccgtgac 240

ccagcgtgcg ggcggcggg atg aga ggg agc cat cgg gcc gcg ccg gcc ctg  292
                  Met Arg Gly Ser His Arg Ala Ala Pro Ala Leu
                    1               5                  10

cgg ccc cgg ggg cgg ctc tgg ccc gtg ctg gcc gtg ctg gcg gcg gcc   340
Arg Pro Arg Gly Arg Leu Trp Pro Val Leu Ala Val Leu Ala Ala Ala
            15                  20                  25

gcc gcg gcg ggc tgt gcc cag gca gcc atg gac gag tgc acg gac gag   388
Ala Ala Ala Gly Cys Ala Gln Ala Ala Met Asp Glu Cys Thr Asp Glu
        30                  35                  40

ggc ggg cgg ccg cag cgc tgc atg ccc gag ttc gtc aac gcc gct ttc   436
Gly Gly Arg Pro Gln Arg Cys Met Pro Glu Phe Val Asn Ala Ala Phe
    45                  50                  55

aac gtg act gtg gtg gcc acc aac acg tgt ggg act ccg ccc gag gaa   484
Asn Val Thr Val Val Ala Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu
60                  65                  70                  75

tac tgt gtg cag acc ggg gtg acc ggg gtc acc aag tcc tgt cac ctg   532
Tyr Cys Val Gln Thr Gly Val Thr Gly Val Thr Lys Ser Cys His Leu
                80                  85                  90

tgc gac gcc ggg cag ccc cac ctg cag cac ggg gca gcc ttc ctg acc   580
Cys Asp Ala Gly Gln Pro His Leu Gln His Gly Ala Ala Phe Leu Thr
            95                  100                 105

gac tac aac aac cag gcc gac acc acc tgg tgg caa agc cag acc atg   628
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Asp Tyr Asn Asn Gln Ala Asp Thr Thr Trp Trp Gln Ser Gln Thr Met
        110                 115                 120

ctg gcc ggg gtg cag tac ccc agc tcc atc aac ctc acg ctg cac ctg   676
Leu Ala Gly Val Gln Tyr Pro Ser Ser Ile Asn Leu Thr Leu His Leu
    125                 130                 135

gga aaa gct ttt gac atc acc tat gtg cgt ctc aag ttc cac acc agc   724
Gly Lys Ala Phe Asp Ile Thr Tyr Val Arg Leu Lys Phe His Thr Ser
140                 145                 150                 155

cgc ccg gag agc ttt gcc att tac aag cgc aca cgg gaa gac ggg ccc   772
Arg Pro Glu Ser Phe Ala Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro
                160                 165                 170

tgg att cct tac cag tac tac agt ggt tcc tgc gag aac acc tac tcc   820
Trp Ile Pro Tyr Gln Tyr Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser
            175                 180                 185

aag gca aac cgc ggc ttc atc agg aca gga ggg gac gag cag cag gcc   868
Lys Ala Asn Arg Gly Phe Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala
        190                 195                 200

ttg tgt act gat gaa ttc agt gac att tct ccc ctc act ggg ggc aac   916
Leu Cys Thr Asp Glu Phe Ser Asp Ile Ser Pro Leu Thr Gly Gly Asn
    205                 210                 215

gtg gcc ttt tct acc ctg gaa gga agg ccc agc gcc tat aac ttt gac   964
Val Ala Phe Ser Thr Leu Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp
220                 225                 230                 235

aat agc cct gtg ctg cag gaa tgg gta act gcc act gac atc aga gta   1012
Asn Ser Pro Val Leu Gln Glu Trp Val Thr Ala Thr Asp Ile Arg Val
                240                 245                 250

act ctt aat cgc ctg aac act ttt gga gat gaa gtg ttt aac gat ccc   1060
Thr Leu Asn Arg Leu Asn Thr Phe Gly Asp Glu Val Phe Asn Asp Pro
            255                 260                 265

aaa gtt ctc aag tcc tat tat tat gcc atc tct gat ttt gct gta ggt   1108
Lys Val Leu Lys Ser Tyr Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly
        270                 275                 280

ggc aga tgt aaa tgt aat gga cac gca agc gag tgt atg aag aac gaa   1156
Gly Arg Cys Lys Cys Asn Gly His Ala Ser Glu Cys Met Lys Asn Glu
    285                 290                 295

ttt gat aag ctg gtg tgt aat tgc aaa cat aac aca tat gga gta gac   1204
Phe Asp Lys Leu Val Cys Asn Cys Lys His Asn Thr Tyr Gly Val Asp
300                 305                 310                 315

tgt gaa aag tgt ctt cct ttc ttc aat gac cgg ccg tgg agg agg gca   1252
Cys Glu Lys Cys Leu Pro Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala
                320                 325                 330

act gcg gaa agt gcc agt gaa tgc ctg ccc tgt gat tgc aat ggt cga   1300
Thr Ala Glu Ser Ala Ser Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg
            335                 340                 345

tcc cag gaa tgc tac ttc gac cct gaa ctc tat cgt tcc act ggc cat   1348
Ser Gln Glu Cys Tyr Phe Asp Pro Glu Leu Tyr Arg Ser Thr Gly His
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        350                 355                 360

ggg ggc cac tgt acc aac tgc cag gat aac aca gat ggc gcc cac tgt   1396
Gly Gly His Cys Thr Asn Cys Gln Asp Asn Thr Asp Gly Ala His Cys
    365                 370                 375

gag agg tgc cga gag aac ttc ttc cgc ctt ggc aac aat gaa gcc tgc   1444
Glu Arg Cys Arg Glu Asn Phe Phe Arg Leu Gly Asn Asn Glu Ala Cys
380                 385                 390                 395

tct tca tgc cac tgt agt cct gtg ggc tct cta agc aca cag tgt gat   1492
Ser Ser Cys His Cys Ser Pro Val Gly Ser Leu Ser Thr Gln Cys Asp
                400                 405                 410

agt tac ggc aga tgc agc tgt aag cca gga gtg atg ggg gac aaa tgt   1540
Ser Tyr Gly Arg Cys Ser Cys Lys Pro Gly Val Met Gly Asp Lys Cys
            415                 420                 425

gac cgt tgc cag cct gga ttc cat tct ctc act gaa gca gga tgc agg   1588
Asp Arg Cys Gln Pro Gly Phe His Ser Leu Thr Glu Ala Gly Cys Arg
        430                 435                 440

cca tgc tct tgt gat ccc tct ggc agc ata gat gaa tgt aat gtt gaa   1636
Pro Cys Ser Cys Asp Pro Ser Gly Ser Ile Asp Glu Cys Asn Val Glu
    445                 450                 455

aca gga aga tgt gtt tgc aaa gac aat gtc gaa ggc ttc aat tgt gaa   1684
Thr Gly Arg Cys Val Cys Lys Asp Asn Val Glu Gly Phe Asn Cys Glu
460                 465                 470                 475

aga tgc aaa cct gga ttt ttt aat ctg gaa tca tct aat cct cgg ggt   1732
Arg Cys Lys Pro Gly Phe Phe Asn Leu Glu Ser Ser Asn Pro Arg Gly
                480                 485                 490

tgc aca ccc tgc ttc tgc ttt ggg cat tct tct gtc tgt aca aac gct   1780
Cys Thr Pro Cys Phe Cys Phe Gly His Ser Ser Val Cys Thr Asn Ala
            495                 500                 505

gtt ggc tac agt gtt tat tct atc tcc tct acc ttt cag att gat gag   1828
Val Gly Tyr Ser Val Tyr Ser Ile Ser Ser Thr Phe Gln Ile Asp Glu
        510                 515                 520

gat ggg tgg cgt gcg gaa cag aga gat ggc tct gaa gca tct ctc gag   1876
Asp Gly Trp Arg Ala Glu Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu
    525                 530                 535

tgg tcc tct gag agg caa gat atc gcc gtg atc tca gac agc tac ttt   1924
Trp Ser Ser Glu Arg Gln Asp Ile Ala Val Ile Ser Asp Ser Tyr Phe
540                 545                 550                 555

cct cgg tac ttc att gct cct gca aag ttc ttg ggc aag cag gtg ttg   1972
Pro Arg Tyr Phe Ile Ala Pro Ala Lys Phe Leu Gly Lys Gln Val Leu
                560                 565                 570

agt tat ggt cag aac ctc tcc ttc tcc ttt cga gtg gac agg cga gat   2020
Ser Tyr Gly Gln Asn Leu Ser Phe Ser Phe Arg Val Asp Arg Arg Asp
            575                 580                 585

act cgc ctc tct gcc gaa gac ctt gtg ctt gag gga gct ggc tta aga   2068
Thr Arg Leu Ser Ala Glu Asp Leu Val Leu Glu Gly Ala Gly Leu Arg
        590                 595                 600
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gta tct gta ccc ttg atc gct cag ggc aat tcc tat cca agt gag acc   2116
Val Ser Val Pro Leu Ile Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr
    605                 610                 615

act gtg aag tat gtc ttc agg ctc cat gaa gca aca gat tac cct tgg   2164
Thr Val Lys Tyr Val Phe Arg Leu His Glu Ala Thr Asp Tyr Pro Trp
620                 625                 630                 635

agg cct gct ctt acc cct ttt gaa ttt cag aag ctc cta aac aac ttg   2212
Arg Pro Ala Leu Thr Pro Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu
                640                 645                 650

acc tct atc aag ata cgt ggg aca tac agt gag aga agt gct gga tat   2260
Thr Ser Ile Lys Ile Arg Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr
            655                 660                 665

ttg gat gat gtc acc ctg gca agt gct cgt cct ggg cct gga gtc cct   2308
Leu Asp Asp Val Thr Leu Ala Ser Ala Arg Pro Gly Pro Gly Val Pro
        670                 675                 680

gca act tgg gtg gag tcc tgc acc tgt cct gtg gga tat gga ggg cag   2356
Ala Thr Trp Val Glu Ser Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln
    685                 690                 695

ttt tgt gag atg tgc ctc tca ggt tac aga aga gaa act cct aat ctt   2404
Phe Cys Glu Met Cys Leu Ser Gly Tyr Arg Arg Glu Thr Pro Asn Leu
700                 705                 710                 715

gga cca tac agt cca tgt gtg ctt tgc gcc tgc aat gga cac agc gag   2452
Gly Pro Tyr Ser Pro Cys Val Leu Cys Ala Cys Asn Gly His Ser Glu
                720                 725                 730

acc tgt gat cct gag aca ggt gtt tgt aac tgc aga gac aat acg gct   2500
Thr Cys Asp Pro Glu Thr Gly Val Cys Asn Cys Arg Asp Asn Thr Ala
            735                 740                 745

ggc ccg cac tgt gag aag tgc agt gat ggg tac tat gga gat tca act   2548
Gly Pro His Cys Glu Lys Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr
        750                 755                 760

gca ggc acc tcc tcc gat tgc caa ccc tgt ccg tgt cct gga ggt tca   2596
Ala Gly Thr Ser Ser Asp Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser
    765                 770                 775

agt tgt gct gtt gtt ccc aag aca aag gag gtg gtg tgc acc aac tgt   2644
Ser Cys Ala Val Val Pro Lys Thr Lys Glu Val Val Cys Thr Asn Cys
780                 785                 790                 795

cct act ggc acc act ggt aag aga tgt gag ctc tgt gat gat ggc tac   2692
Pro Thr Gly Thr Thr Gly Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr
                800                 805                 810

ttt gga gac ccc ctg ggt aga aac ggc cct gtg aga ctt tgc cgc ctg   2740
Phe Gly Asp Pro Leu Gly Arg Asn Gly Pro Val Arg Leu Cys Arg Leu
            815                 820                 825

tgc cag tgc agt gac aac atc gat ccc aac gca gtt gga aat tgc aat   2788
Cys Gln Cys Ser Asp Asn Ile Asp Pro Asn Ala Val Gly Asn Cys Asn
        830                 835                 840
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cgc ttg acg gga gaa tgc ctg aag tgc atc tat aac act gct ggc ttc   2836
Arg Leu Thr Gly Glu Cys Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe
    845                 850                 855

tat tgt gac cgg tgc aaa gac gga ttt ttt gga aat ccc ctg gct ccc   2884
Tyr Cys Asp Arg Cys Lys Asp Gly Phe Phe Gly Asn Pro Leu Ala Pro
860                 865                 870                 875

aat cca gca gac aaa tgc aaa gcc tgc aat tgc aat ccg tat ggg acc   2932
Asn Pro Ala Asp Lys Cys Lys Ala Cys Asn Cys Asn Pro Tyr Gly Thr
                880                 885                 890

atg aag cag cag agc agc tgt aac ccc gtg acg ggg cag tgt gaa tgt   2980
Met Lys Gln Gln Ser Ser Cys Asn Pro Val Thr Gly Gln Cys Glu Cys
            895                 900                 905

ttg cct cac gtg act ggc cag gac tgt ggt gct tgt gac cct gga ttc   3028
Leu Pro His Val Thr Gly Gln Asp Cys Gly Ala Cys Asp Pro Gly Phe
        910                 915                 920

tac aat ctg cag agt ggg caa ggc tgt gag agg tgt gac tgc cat gcc   3076
Tyr Asn Leu Gln Ser Gly Gln Gly Cys Glu Arg Cys Asp Cys His Ala
    925                 930                 935

ttg ggc tcc acc aat ggg cag tgt gac atc cgc acc ggc cag tgt gag   3124
Leu Gly Ser Thr Asn Gly Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu
940                 945                 950                 955

tgc cag ccc ggc atc act ggt cag cac tgt gag cgc tgt gag gtc aac   3172
Cys Gln Pro Gly Ile Thr Gly Gln His Cys Glu Arg Cys Glu Val Asn
                960                 965                 970

cac ttt ggg ttt gga cct gaa ggc tgc aaa ccc tgt gac tgt cat cct   3220
His Phe Gly Phe Gly Pro Glu Gly Cys Lys Pro Cys Asp Cys His Pro
            975                 980                 985

gag gga tct ctt tca ctt cag tgc aaa gat gat ggt cgc tgt gaa tgc   3268
Glu Gly Ser Leu Ser Leu Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys
        990                 995                1000

aga gaa ggc ttt gtg gga aat cgc tgt gac cag tgt gaa gaa aac tat   3316
Arg Glu Gly Phe Val Gly Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr
   1005                1010                1015

ttc tac aat cgg tct tgg cct ggc tgc cag gaa tgt cca gct tgt tac   3364
Phe Tyr Asn Arg Ser Trp Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr
1020                1025                1030                1035

cgg ctg gta aag gat aag gtt gct gat cat aga gtg aag ctc cag gaa   3412
Arg Leu Val Lys Asp Lys Val Ala Asp His Arg Val Lys Leu Gln Glu
               1040                1045                1050

tta gag agt ctc ata gca aac ctt gga act ggg gat gag atg gtg aca   3460
Leu Glu Ser Leu Ile Ala Asn Leu Gly Thr Gly Asp Glu Met Val Thr
           1055                1060                1065

gat caa gcc ttc gag gat aga cta aag gaa gca gag agg gaa gtt atg   3508
Asp Gln Ala Phe Glu Asp Arg Leu Lys Glu Ala Glu Arg Glu Val Met
       1070                1075                1080

gac ctc ctt cgt gag gcc cag gat gtc aaa gat gtt gac cag aat ttg   3556
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Asp Leu Leu Arg Glu Ala Gln Asp Val Lys Asp Val Asp Gln Asn Leu
   1085                1090                1095

atg gat cgc cta cag aga gtg aat aac act ctg tcc agc caa att agc   3604
Met Asp Arg Leu Gln Arg Val Asn Asn Thr Leu Ser Ser Gln Ile Ser
1100                1105                1110                1115

cgt tta cag aat atc cgg aat acc att gaa gag act gga aac ttg gct   3652
Arg Leu Gln Asn Ile Arg Asn Thr Ile Glu Glu Thr Gly Asn Leu Ala
                1120                1125                1130

gaa caa gcg cgt gcc cat gta gag aac aca gag cgg ttg att gaa atc   3700
Glu Gln Ala Arg Ala His Val Glu Asn Thr Glu Arg Leu Ile Glu Ile
            1135                1140                1145

gca tcc aga gaa ctt gag aaa gca aaa gtc gct gct gcc aat gtg tca   3748
Ala Ser Arg Glu Leu Glu Lys Ala Lys Val Ala Ala Ala Asn Val Ser
        1150                1155                1160

gtc act cag cca gaa tct aca ggg gac cca aac aac atg act ctt ttg   3796
Val Thr Gln Pro Glu Ser Thr Gly Asp Pro Asn Asn Met Thr Leu Leu
    1165                1170                1175

gca gaa gag gct cga aag ctt gct gaa cgt cat aaa cag gaa gct gat   3844
Ala Glu Glu Ala Arg Lys Leu Ala Glu Arg His Lys Gln Glu Ala Asp
1180                1185                1190                1195

gac att gtt cga gtg gca aag aca gcc aat gat acg tca act gag gca   3892
Asp Ile Val Arg Val Ala Lys Thr Ala Asn Asp Thr Ser Thr Glu Ala
                1200                1205                1210

tac aac ctg ctt ctg agg aca ctg gca gga gaa aat caa aca gca ttt   3940
Tyr Asn Leu Leu Leu Arg Thr Leu Ala Gly Glu Asn Gln Thr Ala Phe
            1215                1220                1225

gag att gaa gag ctt aat agg aag tat gaa caa gcg aag aac atc tca   3988
Glu Ile Glu Glu Leu Asn Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser
        1230                1235                1240

cag gat ctg gaa aaa caa gct gcc cga gta cat gag gag gcc aaa agg   4036
Gln Asp Leu Glu Lys Gln Ala Ala Arg Val His Glu Glu Ala Lys Arg
    1245                1250                1255

gcc ggt gac aaa gct gtg gag atc tat gcc agc gtg gct cag ctg agc   4084
Ala Gly Asp Lys Ala Val Glu Ile Tyr Ala Ser Val Ala Gln Leu Ser
1260                1265                1270                1275

cct ttg gac tct gag aca ctg gag aat gaa gca aat aac ata aag atg   4132
Pro Leu Asp Ser Glu Thr Leu Glu Asn Glu Ala Asn Asn Ile Lys Met
                1280                1285                1290

gaa gct gag aat ctg gaa caa ctg att gac cag aaa tta aaa gat tat   4180
Glu Ala Glu Asn Leu Glu Gln Leu Ile Asp Gln Lys Leu Lys Asp Tyr
            1295                1300                1305

gag gac ctc aga gaa gat atg aga ggg aag gaa ctt gaa gtc aag aac   4228
Glu Asp Leu Arg Glu Asp Met Arg Gly Lys Glu Leu Glu Val Lys Asn
        1310                1315                1320

ctt ctg gag aaa ggc aag act gaa cag cag acc gca gac caa ctc cta   4276
Leu Leu Glu Lys Gly Lys Thr Glu Gln Gln Thr Ala Asp Gln Leu Leu
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   1325                1330                1335

gcc cga gct gat gct gcc aag gcc ctc gct gaa gaa gct gca aag aag   4324
Ala Arg Ala Asp Ala Ala Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys
1340                1345                1350                1355

gga cgg gat acc tta caa gaa gct aat gac att ctc aac aac ctg aaa   4372
Gly Arg Asp Thr Leu Gln Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys
                1360                1365                1370

gat ttt gat agg cgc gtg aac gat aac aag acg gcc gca gag gag gca   4420
Asp Phe Asp Arg Arg Val Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala
           1375                1380                1385

cta agg aag att cct gcc atc aac cag acc atc act gaa gcc aat gaa   4468
Leu Arg Lys Ile Pro Ala Ile Asn Gln Thr Ile Thr Glu Ala Asn Glu
       1390                1395                1400

aag acc aga gaa gcc cag cag gcc ctg ggc agt gct gcg gcg gat gcc   4516
Lys Thr Arg Glu Ala Gln Gln Ala Leu Gly Ser Ala Ala Ala Asp Ala
   1405                1410                1415

aca gag gcc aag aac aag gcc cat gag gcg gag agg atc gca agc gct   4564
Thr Glu Ala Lys Asn Lys Ala His Glu Ala Glu Arg Ile Ala Ser Ala
1420                1425                1430                1435

gtc caa aag aat gcc acc agc acc aag gca gaa gct gaa aga act ttt   4612
Val Gln Lys Asn Ala Thr Ser Thr Lys Ala Glu Ala Glu Arg Thr Phe
                1440                1445                1450

gca gaa gtt aca gat ctg gat aat gag gtg aac aat atg ttg aag caa   4660
Ala Glu Val Thr Asp Leu Asp Asn Glu Val Asn Asn Met Leu Lys Gln
           1455                1460                1465

ctg cag gaa gca gaa aaa gag cta aag aga aaa caa gat gac gct gac   4708
Leu Gln Glu Ala Glu Lys Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp
       1470                1475                1480

cag gac atg atg atg gca ggg atg gct tca cag gct gct caa gaa gcc   4756
Gln Asp Met Met Met Ala Gly Met Ala Ser Gln Ala Ala Gln Glu Ala
   1485                1490                1495

gag atc aat gcc aga aaa gcc aaa aac tct gtt act agc ctc ctc agc   4804
Glu Ile Asn Ala Arg Lys Ala Lys Asn Ser Val Thr Ser Leu Leu Ser
1500                1505                1510                1515

att att aat gac ctc ttg gag cag ctg ggg cag ctg gat aca gtg gac   4852
Ile Ile Asn Asp Leu Leu Glu Gln Leu Gly Gln Leu Asp Thr Val Asp
                1520                1525                1530

ctg aat aag cta aac gag att gaa ggc acc cta aac aaa gcc aaa gat   4900
Leu Asn Lys Leu Asn Glu Ile Glu Gly Thr Leu Asn Lys Ala Lys Asp
           1535                1540                1545

gaa atg aag gtc agc gat ctt gat agg aaa gtg tct gac ctg gag aat   4948
Glu Met Lys Val Ser Asp Leu Asp Arg Lys Val Ser Asp Leu Glu Asn
       1550                1555                1560

gaa gcc aag aag cag gag gct gcc atc atg gac tat aac cga gat atc   4996
Glu Ala Lys Lys Gln Glu Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile
   1565                1570                1575
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gag gag atc atg aag gac att cgc aat ctg gag gac atc agg aag acc   5044
Glu Glu Ile Met Lys Asp Ile Arg Asn Leu Glu Asp Ile Arg Lys Thr
1580                1585                1590                1595

tta cca tct ggc tgc ttc aac acc ccg tcc att gaa aag ccc           5086
Leu Pro Ser Gly Cys Phe Asn Thr Pro Ser Ile Glu Lys Pro
                1600                1605

tagtgtcttt agggctggaa ggcagcatcc ctctgacagg ggggcagttg tgaggccaca 5146

gagtgccttg acacaaagat tacatttttc agacccccac tcctctgctg ctgtccatca 5206

ctgtcctttt gaaccaggaa aagtcacaga gtttaaagag aagcaaatta aacatcctga 5266

atcgggaaca aagggtttta tctaataaag tgtctcttcc                       5306


<210> 22
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<212> PRT
<213> Homo sapiens

<400> 22
Met Arg Gly Ser His Arg Ala Ala Pro Ala Leu Arg Pro Arg Gly Arg
  1               5                  10                  15

Leu Trp Pro Val Leu Ala Val Leu Ala Ala Ala Ala Ala Ala Gly Cys
             20                  25                  30

Ala Gln Ala Ala Met Asp Glu Cys Thr Asp Glu Gly Gly Arg Pro Gln
         35                  40                  45

Arg Cys Met Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val
     50                  55                  60

Ala Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr
 65                  70                  75                  80

Gly Val Thr Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln
                 85                  90                  95

Pro His Leu Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln
            100                 105                 110

Ala Asp Thr Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln
        115                 120                 125

Tyr Pro Ser Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp
    130                 135                 140

Ile Thr Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe
145                 150                 155                 160

Ala Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln
                165                 170                 175

Tyr Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly
            180                 185                 190

Phe Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu
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        195                 200                 205

Phe Ser Asp Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser Thr
    210                 215                 220

Leu Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu
225                 230                 235                 240

Gln Glu Trp Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu
                245                 250                 255

Asn Thr Phe Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser
            260                 265                 270

Tyr Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys
        275                 280                 285

Asn Gly His Ala Ser Glu Cys Met Lys Asn Glu Phe Asp Lys Leu Val
    290                 295                 300

Cys Asn Cys Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu
305                 310                 315                 320

Pro Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala
                325                 330                 335

Ser Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr
            340                 345                 350

Phe Asp Pro Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr
        355                 360                 365

Asn Cys Gln Asp Asn Thr Asp Gly Ala His Cys Glu Arg Cys Arg Glu
    370                 375                 380

Asn Phe Phe Arg Leu Gly Asn Asn Glu Ala Cys Ser Ser Cys His Cys
385                 390                 395                 400

Ser Pro Val Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys
                405                 410                 415

Ser Cys Lys Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro
            420                 425                 430

Gly Phe His Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp
        435                 440                 445

Pro Ser Gly Ser Ile Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val
    450                 455                 460

Cys Lys Asp Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly
465                 470                 475                 480

Phe Phe Asn Leu Glu Ser Ser Asn Pro Arg Gly Cys Thr Pro Cys Phe
                485                 490                 495

Cys Phe Gly His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val
            500                 505                 510

Tyr Ser Ile Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Ala
        515                 520                 525
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Glu Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Glu Arg
    530                 535                 540

Gln Asp Ile Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile
545                 550                 555                 560

Ala Pro Ala Lys Phe Leu Gly Lys Gln Val Leu Ser Tyr Gly Gln Asn
                565                 570                 575

Leu Ser Phe Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala
            580                 585                 590

Glu Asp Leu Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu
        595                 600                 605

Ile Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Val
    610                 615                 620

Phe Arg Leu His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Thr
625                 630                 635                 640

Pro Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile
                645                 650                 655

Arg Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr
            660                 665                 670

Leu Ala Ser Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu
        675                 680                 685

Ser Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Met Cys
    690                 695                 700

Leu Ser Gly Tyr Arg Arg Glu Thr Pro Asn Leu Gly Pro Tyr Ser Pro
705                 710                 715                 720

Cys Val Leu Cys Ala Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu
                725                 730                 735

Thr Gly Val Cys Asn Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu
            740                 745                 750

Lys Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr Ala Gly Thr Ser Ser
        755                 760                 765

Asp Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Val Val
    770                 775                 780

Pro Lys Thr Lys Glu Val Val Cys Thr Asn Cys Pro Thr Gly Thr Thr
785                 790                 795                 800

Gly Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu
                805                 810                 815

Gly Arg Asn Gly Pro Val Arg Leu Cys Arg Leu Cys Gln Cys Ser Asp
            820                 825                 830

Asn Ile Asp Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu
        835                 840                 845
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Cys Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys
    850                 855                 860

Lys Asp Gly Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys
865                 870                 875                 880

Cys Lys Ala Cys Asn Cys Asn Pro Tyr Gly Thr Met Lys Gln Gln Ser
                885                 890                 895

Ser Cys Asn Pro Val Thr Gly Gln Cys Glu Cys Leu Pro His Val Thr
            900                 905                 910

Gly Gln Asp Cys Gly Ala Cys Asp Pro Gly Phe Tyr Asn Leu Gln Ser
        915                 920                 925

Gly Gln Gly Cys Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn
    930                 935                 940

Gly Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile
945                 950                 955                 960

Thr Gly Gln His Cys Glu Arg Cys Glu Val Asn His Phe Gly Phe Gly
                965                 970                 975

Pro Glu Gly Cys Lys Pro Cys Asp Cys His Pro Glu Gly Ser Leu Ser
            980                 985                 990

Leu Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val
        995                1000                1005

Gly Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser
   1010                1015                1020

Trp Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp
025                1030                1035                1040

Lys Val Ala Asp His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile
               1045                1050                1055

Ala Asn Leu Gly Thr Gly Asp Glu Met Val Thr Asp Gln Ala Phe Glu
           1060                1065                1070

Asp Arg Leu Lys Glu Ala Glu Arg Glu Val Met Asp Leu Leu Arg Glu
       1075                1080                1085

Ala Gln Asp Val Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln
   1090                1095                1100

Arg Val Asn Asn Thr Leu Ser Ser Gln Ile Ser Arg Leu Gln Asn Ile
105                1110                1115                1120

Arg Asn Thr Ile Glu Glu Thr Gly Asn Leu Ala Glu Gln Ala Arg Ala
               1125                1130                1135

His Val Glu Asn Thr Glu Arg Leu Ile Glu Ile Ala Ser Arg Glu Leu
           1140                1145                1150

Glu Lys Ala Lys Val Ala Ala Ala Asn Val Ser Val Thr Gln Pro Glu
       1155                1160                1165

Ser Thr Gly Asp Pro Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg
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1170                1175                1180

Lys Leu Ala Glu Arg His Lys Gln Glu Ala Asp Asp Ile Val Arg Val
185                 1190                1195                1200

Ala Lys Thr Ala Asn Asp Thr Ser Thr Glu Ala Tyr Asn Leu Leu Leu
                1205                1210                1215

Arg Thr Leu Ala Gly Glu Asn Gln Thr Ala Phe Glu Ile Glu Glu Leu
            1220                1225                1230

Asn Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys
        1235                1240                1245

Gln Ala Ala Arg Val His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala
    1250                1255                1260

Val Glu Ile Tyr Ala Ser Val Ala Gln Leu Ser Pro Leu Asp Ser Glu
265                 1270                1275                1280

Thr Leu Glu Asn Glu Ala Asn Asn Ile Lys Met Glu Ala Glu Asn Leu
                1285                1290                1295

Glu Gln Leu Ile Asp Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu
            1300                1305                1310

Asp Met Arg Gly Lys Glu Leu Glu Val Lys Asn Leu Leu Glu Lys Gly
        1315                1320                1325

Lys Thr Glu Gln Gln Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala
    1330                1335                1340

Ala Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys Gly Arg Asp Thr Leu
345                 1350                1355                1360

Gln Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg
                1365                1370                1375

Val Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala Leu Arg Lys Ile Pro
            1380                1385                1390

Ala Ile Asn Gln Thr Ile Thr Glu Ala Asn Glu Lys Thr Arg Glu Ala
        1395                1400                1405

Gln Gln Ala Leu Gly Ser Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn
    1410                1415                1420

Lys Ala His Glu Ala Glu Arg Ile Ala Ser Ala Val Gln Lys Asn Ala
425                 1430                1435                1440

Thr Ser Thr Lys Ala Glu Ala Glu Arg Thr Phe Ala Glu Val Thr Asp
                1445                1450                1455

Leu Asp Asn Glu Val Asn Asn Met Leu Lys Gln Leu Gln Glu Ala Glu
            1460                1465                1470

Lys Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met
        1475                1480                1485

Ala Gly Met Ala Ser Gln Ala Ala Gln Glu Ala Glu Ile Asn Ala Arg
    1490                1495                1500
```

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Lys Ala Lys Asn Ser Val Thr Ser Leu Leu Ser Ile Ile Asn Asp Leu
505                 1510                1515                1520

Leu Glu Gln Leu Gly Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn
                1525                1530                1535

Glu Ile Glu Gly Thr Leu Asn Lys Ala Lys Asp Glu Met Lys Val Ser
            1540                1545                1550

Asp Leu Asp Arg Lys Val Ser Asp Leu Glu Asn Glu Ala Lys Lys Gln
        1555                1560                1565

Glu Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile Glu Glu Ile Met Lys
    1570                1575                1580

Asp Ile Arg Asn Leu Glu Asp Ile Arg Lys Thr Leu Pro Ser Gly Cys
585                 1590                1595                1600

Phe Asn Thr Pro Ser Ile Glu Lys Pro
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<210> 23
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<212> DNA
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<400> 23

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cag gca gcc atg gac gag tgc acg gac gag ggc ggg cgg ccg cag cgc   48
Gln Ala Ala Met Asp Glu Cys Thr Asp Glu Gly Gly Arg Pro Gln Arg
  1               5                  10                  15

tgc atg ccc gag ttc gtc aac gcc gct ttc aac gtg act gtg gtg gcc   96
Cys Met Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val Ala
            20                  25                  30

acc aac acg tgt ggg act ccg ccc gag gaa tac tgt gtg cag acc ggg   144
Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr Gly
        35                  40                  45

gtg acc ggg gtc acc aag tcc tgt cac ctg tgc gac gcc ggg cag ccc   192
Val Thr Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln Pro
    50                  55                  60

cac ctg cag cac ggg gca gcc ttc ctg acc gac tac aac aac cag gcc   240
His Leu Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln Ala
65                  70                  75                  80

gac acc acc tgg tgg caa agc cag acc atg ctg gcc ggg gtg cag tac   288
Asp Thr Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln Tyr
                85                  90                  95

ccc agc tcc atc aac ctc acg ctg cac ctg gga aaa gct ttt gac atc   336
Pro Ser Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp Ile
            100                 105                 110
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acc tat gtg cgt ctc aag ttc cac acc agc cgc ccg gag agc ttt gcc   384
Thr Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe Ala
        115                 120                 125

att tac aag cgc aca cgg gaa gac ggg ccc tgg att cct tac cag tac   432
Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln Tyr
    130                 135                 140

tac agt ggt tcc tgc gag aac acc tac tcc aag gca aac cgc ggc ttc   480
Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly Phe
145                 150                 155                 160

atc agg aca gga ggg gac gag cag cag gcc ttg tgt act gat gaa ttc   528
Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu Phe
                165                 170                 175

agt gac att tct ccc ctc act ggg ggc aac gtg gcc ttt tct acc ctg   576
Ser Asp Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser Thr Leu
            180                 185                 190

gaa gga agg ccc agc gcc tat aac ttt gac aat agc cct gtg ctg cag   624
Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu Gln
        195                 200                 205

gaa tgg gta act gcc act gac atc aga gta act ctt aat cgc ctg aac   672
Glu Trp Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu Asn
    210                 215                 220

act ttt gga gat gaa gtg ttt aac gat ccc aaa gtt ctc aag tcc tat   720
Thr Phe Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser Tyr
225                 230                 235                 240

tat tat gcc atc tct gat ttt gct gta ggt ggc aga tgt aaa tgt aat   768
Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys Asn
                245                 250                 255

gga cac gca agc gag tgt atg aag aac gaa ttt gat aag ctg gtg tgt   816
Gly His Ala Ser Glu Cys Met Lys Asn Glu Phe Asp Lys Leu Val Cys
            260                 265                 270

aat tgc aaa cat aac aca tat gga gta gac tgt gaa aag tgt ctt cct   864
Asn Cys Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu Pro
        275                 280                 285

ttc ttc aat gac cgg ccg tgg agg agg gca act gcg gaa agt gcc agt   912
Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala Ser
    290                 295                 300

gaa tgc ctg ccc tgt gat tgc aat ggt cga tcc cag gaa tgc tac ttc   960
Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr Phe
305                 310                 315                 320

gac cct gaa ctc tat cgt tcc act ggc cat ggg ggc cac tgt acc aac   1008
Asp Pro Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr Asn
                325                 330                 335

tgc cag gat aac aca gat ggc gcc cac tgt gag agg tgc cga gag aac   1056
Cys Gln Asp Asn Thr Asp Gly Ala His Cys Glu Arg Cys Arg Glu Asn
            340                 345                 350

ttc ttc cgc ctt ggc aac aat gaa gcc tgc tct tca tgc cac tgt agt   1104
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Phe Phe Arg Leu Gly Asn Asn Glu Ala Cys Ser Ser Cys His Cys Ser
        355                 360                 365

cct gtg ggc tct cta agc aca cag tgt gat agt tac ggc aga tgc agc   1152
Pro Val Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys Ser
    370                 375                 380

tgt aag cca gga gtg atg ggg gac aaa tgt gac cgt tgc cag cct gga   1200
Cys Lys Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro Gly
385                 390                 395                 400

ttc cat tct ctc act gaa gca gga tgc agg cca tgc tct tgt gat ccc   1248
Phe His Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp Pro
                405                 410                 415

tct ggc agc ata gat gaa tgt aat gtt gaa aca gga aga tgt gtt tgc   1296
Ser Gly Ser Ile Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val Cys
            420                 425                 430

aaa gac aat gtc gaa ggc ttc aat tgt gaa aga tgc aaa cct gga ttt   1344
Lys Asp Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly Phe
        435                 440                 445

ttt aat ctg gaa tca tct aat cct cgg ggt tgc aca ccc tgc ttc tgc   1392
Phe Asn Leu Glu Ser Ser Asn Pro Arg Gly Cys Thr Pro Cys Phe Cys
    450                 455                 460

ttt ggg cat tct tct gtc tgt aca aac gct gtt ggc tac agt gtt tat   1440
Phe Gly His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val Tyr
465                 470                 475                 480

tct atc tcc tct acc ttt cag att gat gag gat ggg tgg cgt gcg gaa   1488
Ser Ile Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Ala Glu
                485                 490                 495

cag aga gat ggc tct gaa gca tct ctc gag tgg tcc tct gag agg caa   1536
Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Glu Arg Gln
            500                 505                 510

gat atc gcc gtg atc tca gac agc tac ttt cct cgg tac ttc att gct   1584
Asp Ile Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile Ala
        515                 520                 525

cct gca aag ttc ttg ggc aag cag gtg ttg agt tat ggt cag aac ctc   1632
Pro Ala Lys Phe Leu Gly Lys Gln Val Leu Ser Tyr Gly Gln Asn Leu
    530                 535                 540

tcc ttc tcc ttt cga gtg gac agg cga gat act cgc ctc tct gcc gaa   1680
Ser Phe Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala Glu
545                 550                 555                 560

gac ctt gtg ctt gag gga gct ggc tta aga gta tct gta ccc ttg atc   1728
Asp Leu Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu Ile
                565                 570                 575

gct cag ggc aat tcc tat cca agt gag acc act gtg aag tat gtc ttc   1776
Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Val Phe
            580                 585                 590

agg ctc cat gaa gca aca gat tac cct tgg agg cct gct ctt acc cct   1824
Arg Leu His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Thr Pro
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        595                 600                 605

ttt gaa ttt cag aag ctc cta aac aac ttg acc tct atc aag ata cgt   1872
Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile Arg
    610                 615                 620

ggg aca tac agt gag aga agt gct gga tat ttg gat gat gtc acc ctg   1920
Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr Leu
625                 630                 635                 640

gca agt gct cgt cct ggg cct gga gtc cct gca act tgg gtg gag tcc   1968
Ala Ser Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu Ser
                645                 650                 655

tgc acc tgt cct gtg gga tat gga ggg cag ttt tgt gag atg tgc ctc   2016
Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Met Cys Leu
            660                 665                 670

tca ggt tac aga aga gaa act cct aat ctt gga cca tac agt cca tgt   2064
Ser Gly Tyr Arg Arg Glu Thr Pro Asn Leu Gly Pro Tyr Ser Pro Cys
        675                 680                 685

gtg ctt tgc gcc tgc aat gga cac agc gag acc tgt gat cct gag aca   2112
Val Leu Cys Ala Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu Thr
    690                 695                 700

ggt gtt tgt aac tgc aga gac aat acg gct ggc ccg cac tgt gag aag   2160
Gly Val Cys Asn Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu Lys
705                 710                 715                 720

tgc agt gat ggg tac tat gga gat tca act gca ggc acc tcc tcc gat   2208
Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr Ala Gly Thr Ser Ser Asp
                725                 730                 735

tgc caa ccc tgt ccg tgt cct gga ggt tca agt tgt gct gtt gtt ccc   2256
Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Val Val Pro
            740                 745                 750

aag aca aag gag gtg gtg tgc acc aac tgt cct act ggc acc act ggt   2304
Lys Thr Lys Glu Val Val Cys Thr Asn Cys Pro Thr Gly Thr Thr Gly
        755                 760                 765

aag aga tgt gag ctc tgt gat gat ggc tac ttt gga gac ccc ctg ggt   2352
Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu Gly
    770                 775                 780

aga aac ggc cct gtg aga ctt tgc cgc ctg tgc cag tgc agt gac aac   2400
Arg Asn Gly Pro Val Arg Leu Cys Arg Leu Cys Gln Cys Ser Asp Asn
785                 790                 795                 800

atc gat ccc aac gca gtt gga aat tgc aat cgc ttg acg gga gaa tgc   2448
Ile Asp Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu Cys
                805                 810                 815

ctg aag tgc atc tat aac act gct ggc ttc tat tgt gac cgg tgc aaa   2496
Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys Lys
            820                 825                 830

gac gga ttt ttt gga aat ccc ctg gct ccc aat cca gca gac aaa tgc   2544
Asp Gly Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys
        835                 840                 845
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aaa gcc tgc aat tgc aat ccg tat ggg acc atg aag cag cag agc agc   2592
Lys Ala Cys Asn Cys Asn Pro Tyr Gly Thr Met Lys Gln Gln Ser Ser
    850                 855                 860

tgt aac ccc gtg acg ggg cag tgt gaa tgt ttg cct cac gtg act ggc   2640
Cys Asn Pro Val Thr Gly Gln Cys Glu Cys Leu Pro His Val Thr Gly
865                 870                 875                 880

cag gac tgt ggt gct tgt gac cct gga ttc tac aat ctg cag agt ggg   2688
Gln Asp Cys Gly Ala Cys Asp Pro Gly Phe Tyr Asn Leu Gln Ser Gly
                885                 890                 895

caa ggc tgt gag agg tgt gac tgc cat gcc ttg ggc tcc acc aat ggg   2736
Gln Gly Cys Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn Gly
            900                 905                 910

cag tgt gac atc cgc acc ggc cag tgt gag tgc cag ccc ggc atc act   2784
Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile Thr
        915                 920                 925

ggt cag cac tgt gag cgc tgt gag gtc aac cac ttt ggg ttt gga cct   2832
Gly Gln His Cys Glu Arg Cys Glu Val Asn His Phe Gly Phe Gly Pro
    930                 935                 940

gaa ggc tgc aaa ccc tgt gac tgt cat cct gag gga tct ctt tca ctt   2880
Glu Gly Cys Lys Pro Cys Asp Cys His Pro Glu Gly Ser Leu Ser Leu
945                 950                 955                 960

cag tgc aaa gat gat ggt cgc tgt gaa tgc aga gaa ggc ttt gtg gga   2928
Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val Gly
                965                 970                 975

aat cgc tgt gac cag tgt gaa gaa aac tat ttc tac aat cgg tct tgg   2976
Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser Trp
            980                 985                 990

cct ggc tgc cag gaa tgt cca gct tgt tac cgg ctg gta aag gat aag   3024
Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp Lys
        995                1000                1005

gtt gct gat cat aga gtg aag ctc cag gaa tta gag agt ctc ata gca   3072
Val Ala Asp His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile Ala
   1010                1015                1020

aac ctt gga act ggg gat gag atg gtg aca gat caa gcc ttc gag gat   3120
Asn Leu Gly Thr Gly Asp Glu Met Val Thr Asp Gln Ala Phe Glu Asp
1025                1030                1035                1040

aga cta aag gaa gca gag agg gaa gtt atg gac ctc ctt cgt gag gcc   3168
Arg Leu Lys Glu Ala Glu Arg Glu Val Met Asp Leu Leu Arg Glu Ala
                1045                1050                1055

cag gat gtc aaa gat gtt gac cag aat ttg atg gat cgc cta cag aga   3216
Gln Asp Val Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln Arg
            1060                1065                1070

gtg aat aac act ctg tcc agc caa att agc cgt tta cag aat atc cgg   3264
Val Asn Asn Thr Leu Ser Ser Gln Ile Ser Arg Leu Gln Asn Ile Arg
        1075                1080                1085
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aat acc att gaa gag act gga aac ttg gct gaa caa gcg cgt gcc cat   3312
Asn Thr Ile Glu Glu Thr Gly Asn Leu Ala Glu Gln Ala Arg Ala His
   1090                1095                1100

gta gag aac aca gag cgg ttg att gaa atc gca tcc aga gaa ctt gag   3360
Val Glu Asn Thr Glu Arg Leu Ile Glu Ile Ala Ser Arg Glu Leu Glu
1105                1110                1115                1120

aaa gca aaa gtc gct gct gcc aat gtg tca gtc act cag cca gaa tct   3408
Lys Ala Lys Val Ala Ala Ala Asn Val Ser Val Thr Gln Pro Glu Ser
               1125                1130                1135

aca ggg gac cca aac aac atg act ctt ttg gca gaa gag gct cga aag   3456
Thr Gly Asp Pro Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Lys
          1140                1145                1150

ctt gct gaa cgt cat aaa cag gaa gct gat gac att gtt cga gtg gca   3504
Leu Ala Glu Arg His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala
       1155                1160                1165

aag aca gcc aat gat acg tca act gag gca tac aac ctg ctt ctg agg   3552
Lys Thr Ala Asn Asp Thr Ser Thr Glu Ala Tyr Asn Leu Leu Leu Arg
   1170                1175                1180

aca ctg gca gga gaa aat caa aca gca ttt gag att gaa gag ctt aat   3600
Thr Leu Ala Gly Glu Asn Gln Thr Ala Phe Glu Ile Glu Glu Leu Asn
1185                1190                1195                1200

agg aag tat gaa caa gcg aag aac atc tca cag gat ctg gaa aaa caa   3648
Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln
               1205                1210                1215

gct gcc cga gta cat gag gag gcc aaa agg gcc ggt gac aaa gct gtg   3696
Ala Ala Arg Val His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val
          1220                1225                1230

gag atc tat gcc agc gtg gct cag ctg agc cct ttg gac tct gag aca   3744
Glu Ile Tyr Ala Ser Val Ala Gln Leu Ser Pro Leu Asp Ser Glu Thr
       1235                1240                1245

ctg gag aat gaa gca aat aac ata aag atg gaa gct gag aat ctg gaa   3792
Leu Glu Asn Glu Ala Asn Asn Ile Lys Met Glu Ala Glu Asn Leu Glu
   1250                1255                1260

caa ctg att gac cag aaa tta aaa gat tat gag gac ctc aga gaa gat   3840
Gln Leu Ile Asp Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp
1265                1270                1275                1280

atg aga ggg aag gaa ctt gaa gtc aag aac ctt ctg gag aaa ggc aag   3888
Met Arg Gly Lys Glu Leu Glu Val Lys Asn Leu Leu Glu Lys Gly Lys
               1285                1290                1295

act gaa cag cag acc gca gac caa ctc cta gcc cga gct gat gct gcc   3936
Thr Glu Gln Gln Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala
          1300                1305                1310

aag gcc ctc gct gaa gaa gct gca aag aag gga cgg gat acc tta caa   3984
Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys Gly Arg Asp Thr Leu Gln
       1315                1320                1325

gaa gct aat gac att ctc aac aac ctg aaa gat ttt gat agg cgc gtg   4032
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Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val
   1330                1335                1340

aac gat aac aag acg gcc gca gag gag gca cta agg aag att cct gcc   4080
Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala Leu Arg Lys Ile Pro Ala
1345                1350                1355                1360

atc aac cag acc atc act gaa gcc aat gaa aag acc aga gaa gcc cag   4128
Ile Asn Gln Thr Ile Thr Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln
                1365                1370                1375

cag gcc ctg ggc agt gct gcg gcg gat gcc aca gag gcc aag aac aag   4176
Gln Ala Leu Gly Ser Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys
           1380                1385                1390

gcc cat gag gcg gag agg atc gca agc gct gtc caa aag aat gcc acc   4224
Ala His Glu Ala Glu Arg Ile Ala Ser Ala Val Gln Lys Asn Ala Thr
       1395                1400                1405

agc acc aag gca gaa gct gaa aga act ttt gca gaa gtt aca gat ctg   4272
Ser Thr Lys Ala Glu Ala Glu Arg Thr Phe Ala Glu Val Thr Asp Leu
   1410                1415                1420

gat aat gag gtg aac aat atg ttg aag caa ctg cag gaa gca gaa aaa   4320
Asp Asn Glu Val Asn Asn Met Leu Lys Gln Leu Gln Glu Ala Glu Lys
1425                1430                1435                1440

gag cta aag aga aaa caa gat gac gct gac cag gac atg atg atg gca   4368
Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala
                1445                1450                1455

ggg atg gct tca cag gct gct caa gaa gcc gag atc aat gcc aga aaa   4416
Gly Met Ala Ser Gln Ala Ala Gln Glu Ala Glu Ile Asn Ala Arg Lys
           1460                1465                1470

gcc aaa aac tct gtt act agc ctc ctc agc att att aat gac ctc ttg   4464
Ala Lys Asn Ser Val Thr Ser Leu Leu Ser Ile Ile Asn Asp Leu Leu
       1475                1480                1485

gag cag ctg ggg cag ctg gat aca gtg gac ctg aat aag cta aac gag   4512
Glu Gln Leu Gly Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu
   1490                1495                1500

att gaa ggc acc cta aac aaa gcc aaa gat gaa atg aag gtc agc gat   4560
Ile Glu Gly Thr Leu Asn Lys Ala Lys Asp Glu Met Lys Val Ser Asp
1505                1510                1515                1520

ctt gat agg aaa gtg tct gac ctg gag aat gaa gcc aag aag cag gag   4608
Leu Asp Arg Lys Val Ser Asp Leu Glu Asn Glu Ala Lys Lys Gln Glu
                1525                1530                1535

gct gcc atc atg gac tat aac cga gat atc gag gag atc atg aag gac   4656
Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile Glu Glu Ile Met Lys Asp
           1540                1545                1550

att cgc aat ctg gag gac atc agg aag acc tta cca tct ggc tgc ttc   4704
Ile Arg Asn Leu Glu Asp Ile Arg Lys Thr Leu Pro Ser Gly Cys Phe
       1555                1560                1565

aac acc ccg tcc att gaa aag ccc tagtgtcttt agggctggaa ggcagcatcc  4758
Asn Thr Pro Ser Ile Glu Lys Pro
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1570 1575

ctctgacagg ggggcagttg tgaggccaca gagtgccttg acacaaagat tacatttttc 4818

agacccccac tcctctgctg ctgtccatca ctgtcctttt gaaccaggaa aagtcacaga 4878

gtttaaagag aagcaaatta aacatcctga atcgggaaca aagggtttta tctaataaag 4938

tgtctcttcc 4948

<210> 24
<211> 1576
<212> PRT
<213> Homo sapiens

<400> 24

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Gln Ala Ala Met Asp Glu Cys Thr Asp Glu Gly Gly Arg Pro Gln Arg
  1               5                  10                  15

Cys Met Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val Ala
             20                  25                  30

Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr Gly
         35                  40                  45

Val Thr Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln Pro
     50                  55                  60

His Leu Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln Ala
 65                  70                  75                  80

Asp Thr Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln Tyr
                 85                  90                  95

Pro Ser Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp Ile
            100                 105                 110

Thr Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe Ala
        115                 120                 125

Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln Tyr
    130                 135                 140

Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly Phe
145                 150                 155                 160

Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu Phe
                165                 170                 175

Ser Asp Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser Thr Leu
            180                 185                 190

Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu Gln
        195                 200                 205

Glu Trp Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu Asn
    210                 215                 220

Thr Phe Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser Tyr
225                 230                 235                 240
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Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys Asn
                245                 250                 255

Gly His Ala Ser Glu Cys Met Lys Asn Glu Phe Asp Lys Leu Val Cys
            260                 265                 270

Asn Cys Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu Pro
        275                 280                 285

Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala Ser
    290                 295                 300

Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr Phe
305                 310                 315                 320

Asp Pro Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr Asn
                325                 330                 335

Cys Gln Asp Asn Thr Asp Gly Ala His Cys Glu Arg Cys Arg Glu Asn
            340                 345                 350

Phe Phe Arg Leu Gly Asn Asn Glu Ala Cys Ser Ser Cys His Cys Ser
        355                 360                 365

Pro Val Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys Ser
    370                 375                 380

Cys Lys Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro Gly
385                 390                 395                 400

Phe His Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp Pro
                405                 410                 415

Ser Gly Ser Ile Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val Cys
            420                 425                 430

Lys Asp Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly Phe
        435                 440                 445

Phe Asn Leu Glu Ser Ser Asn Pro Arg Gly Cys Thr Pro Cys Phe Cys
    450                 455                 460

Phe Gly His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val Tyr
465                 470                 475                 480

Ser Ile Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Ala Glu
                485                 490                 495

Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Glu Arg Gln
            500                 505                 510

Asp Ile Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile Ala
        515                 520                 525

Pro Ala Lys Phe Leu Gly Lys Gln Val Leu Ser Tyr Gly Gln Asn Leu
    530                 535                 540

Ser Phe Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala Glu
545                 550                 555                 560
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Asp Leu Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu Ile
                565                 570                 575

Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Val Phe
            580                 585                 590

Arg Leu His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Thr Pro
        595                 600                 605

Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile Arg
    610                 615                 620

Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr Leu
625                 630                 635                 640

Ala Ser Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu Ser
                645                 650                 655

Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Met Cys Leu
            660                 665                 670

Ser Gly Tyr Arg Arg Glu Thr Pro Asn Leu Gly Pro Tyr Ser Pro Cys
        675                 680                 685

Val Leu Cys Ala Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu Thr
    690                 695                 700

Gly Val Cys Asn Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu Lys
705                 710                 715                 720

Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr Ala Gly Thr Ser Ser Asp
                725                 730                 735

Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Val Val Pro
            740                 745                 750

Lys Thr Lys Glu Val Val Cys Thr Asn Cys Pro Thr Gly Thr Thr Gly
        755                 760                 765

Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu Gly
    770                 775                 780

Arg Asn Gly Pro Val Arg Leu Cys Arg Leu Cys Gln Cys Ser Asp Asn
785                 790                 795                 800

Ile Asp Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu Cys
                805                 810                 815

Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys Lys
            820                 825                 830

Asp Gly Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys
        835                 840                 845

Lys Ala Cys Asn Cys Asn Pro Tyr Gly Thr Met Lys Gln Gln Ser Ser
    850                 855                 860

Cys Asn Pro Val Thr Gly Gln Cys Glu Cys Leu Pro His Val Thr Gly
865                 870                 875                 880

Gln Asp Cys Gly Ala Cys Asp Pro Gly Phe Tyr Asn Leu Gln Ser Gly
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                885                 890                 895

Gln Gly Cys Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn Gly
            900                 905                 910

Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile Thr
        915                 920                 925

Gly Gln His Cys Glu Arg Cys Glu Val Asn His Phe Gly Phe Gly Pro
    930                 935                 940

Glu Gly Cys Lys Pro Cys Asp Cys His Pro Glu Gly Ser Leu Ser Leu
945                 950                 955                 960

Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val Gly
                965                 970                 975

Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser Trp
            980                 985                 990

Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp Lys
        995                1000                1005

Val Ala Asp His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile Ala
   1010                1015                1020

Asn Leu Gly Thr Gly Asp Glu Met Val Thr Asp Gln Ala Phe Glu Asp
1025                1030                1035                1040

Arg Leu Lys Glu Ala Glu Arg Glu Val Met Asp Leu Leu Arg Glu Ala
                1045                1050                1055

Gln Asp Val Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln Arg
           1060                1065                1070

Val Asn Asn Thr Leu Ser Ser Gln Ile Ser Arg Leu Gln Asn Ile Arg
       1075                1080                1085

Asn Thr Ile Glu Glu Thr Gly Asn Leu Ala Glu Gln Ala Arg Ala His
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Val Glu Asn Thr Glu Arg Leu Ile Glu Ile Ala Ser Arg Glu Leu Glu
1105                1110                1115                1120

Lys Ala Lys Val Ala Ala Ala Asn Val Ser Val Thr Gln Pro Glu Ser
                1125                1130                1135

Thr Gly Asp Pro Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Lys
           1140                1145                1150

Leu Ala Glu Arg His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala
       1155                1160                1165

Lys Thr Ala Asn Asp Thr Ser Thr Glu Ala Tyr Asn Leu Leu Leu Arg
   1170                1175                1180

Thr Leu Ala Gly Glu Asn Gln Thr Ala Phe Glu Ile Glu Glu Leu Asn
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Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln
                1205                1210                1215
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Ala Ala Arg Val His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val
          1220                1225                1230

Glu Ile Tyr Ala Ser Val Ala Gln Leu Ser Pro Leu Asp Ser Glu Thr
       1235                1240                1245

Leu Glu Asn Glu Ala Asn Asn Ile Lys Met Glu Ala Glu Asn Leu Glu
   1250                1255                1260

Gln Leu Ile Asp Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp
1265                1270                1275                1280

Met Arg Gly Lys Glu Leu Glu Val Lys Asn Leu Leu Glu Lys Gly Lys
               1285                1290                1295

Thr Glu Gln Gln Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala
          1300                1305                1310

Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys Gly Arg Asp Thr Leu Gln
       1315                1320                1325

Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val
   1330                1335                1340

Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala Leu Arg Lys Ile Pro Ala
1345                1350                1355                1360

Ile Asn Gln Thr Ile Thr Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln
               1365                1370                1375

Gln Ala Leu Gly Ser Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys
          1380                1385                1390

Ala His Glu Ala Glu Arg Ile Ala Ser Ala Val Gln Lys Asn Ala Thr
       1395                1400                1405

Ser Thr Lys Ala Glu Ala Glu Arg Thr Phe Ala Glu Val Thr Asp Leu
   1410                1415                1420

Asp Asn Glu Val Asn Asn Met Leu Lys Gln Leu Gln Glu Ala Glu Lys
1425                1430                1435                1440

Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala
               1445                1450                1455

Gly Met Ala Ser Gln Ala Ala Gln Glu Ala Glu Ile Asn Ala Arg Lys
          1460                1465                1470

Ala Lys Asn Ser Val Thr Ser Leu Leu Ser Ile Ile Asn Asp Leu Leu
       1475                1480                1485

Glu Gln Leu Gly Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu
   1490                1495                1500

Ile Glu Gly Thr Leu Asn Lys Ala Lys Asp Glu Met Lys Val Ser Asp
1505                1510                1515                1520

Leu Asp Arg Lys Val Ser Asp Leu Glu Asn Glu Ala Lys Lys Gln Glu
               1525                1530                1535
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Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile Glu Glu Ile Met Lys Asp
          1540                1545                1550

Ile Arg Asn Leu Glu Asp Ile Arg Lys Thr Leu Pro Ser Gly Cys Phe
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Asn Thr Pro Ser Ile Glu Lys Pro
   1570                1575


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cgccgccacc gcccgcgccg gagtcaggcc cctgggcccc caggctcaag cagcgaagcg 180

gcctccgggg gacgccgcta ggcgagagga acgcgccggt gcccttgcct tcgccgtgac 240

ccagcgtgcg ggcggcggg atg aga ggg agc cat cgg gcc gcg ccg gcc ctg  292
                  Met Arg Gly Ser His Arg Ala Ala Pro Ala Leu
                    1               5                  10

cgg ccc cgg ggg cgg ctc tgg ccc gtg ctg gcc gtg ctg gcg gcg gcc   340
Arg Pro Arg Gly Arg Leu Trp Pro Val Leu Ala Val Leu Ala Ala Ala
            15                  20                  25

gcc gcg gcg ggc tgt gcc cag gca gcc atg gac gag tgc acg gac gag   388
Ala Ala Ala Gly Cys Ala Gln Ala Ala Met Asp Glu Cys Thr Asp Glu
        30                  35                  40

ggc ggg cgg ccg cag cgc tgc atg ccc gag ttc gtc aac gcc gct ttc   436
Gly Gly Arg Pro Gln Arg Cys Met Pro Glu Phe Val Asn Ala Ala Phe
    45                  50                  55

aac gtg act gtg gtg gcc acc aac acg tgt ggg act ccg ccc gag gaa   484
Asn Val Thr Val Val Ala Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu
60                  65                  70                  75

tac tgt gtg cag acc ggg gtg acc ggg gtc acc aag tcc tgt cac ctg   532
Tyr Cys Val Gln Thr Gly Val Thr Gly Val Thr Lys Ser Cys His Leu
                80                  85                  90

tgc gac gcc ggg cag ccc cac ctg cag cac ggg gca gcc ttc ctg acc   580
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Cys Asp Ala Gly Gln Pro His Leu Gln His Gly Ala Ala Phe Leu Thr
                95                  100                 105

gac tac aac aac cag gcc gac acc acc tgg tgg caa agc cag acc atg   628
Asp Tyr Asn Asn Gln Ala Asp Thr Thr Trp Trp Gln Ser Gln Thr Met
        110                 115                 120

ctg gcc ggg gtg cag tac ccc agc tcc atc aac ctc acg ctg cac ctg   676
Leu Ala Gly Val Gln Tyr Pro Ser Ser Ile Asn Leu Thr Leu His Leu
    125                 130                 135

gga aaa gct ttt gac atc acc tat gtg cgt ctc aag ttc cac acc agc   724
Gly Lys Ala Phe Asp Ile Thr Tyr Val Arg Leu Lys Phe His Thr Ser
140                 145                 150                 155

cgc ccg gag agc ttt gcc att tac aag cgc aca cgg gaa gac ggg ccc   772
Arg Pro Glu Ser Phe Ala Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro
                160                 165                 170

tgg att cct tac cag tac tac agt ggt tcc tgc gag aac acc tac tcc   820
Trp Ile Pro Tyr Gln Tyr Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser
            175                 180                 185

aag gca aac cgc ggc ttc atc agg aca gga ggg gac gag cag cag gcc   868
Lys Ala Asn Arg Gly Phe Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala
        190                 195                 200

ttg tgt act gat gaa ttc agt gac att tct ccc ctc act ggg ggc aac   916
Leu Cys Thr Asp Glu Phe Ser Asp Ile Ser Pro Leu Thr Gly Gly Asn
    205                 210                 215

gtg gcc ttt tct acc ctg gaa gga agg ccc agc gcc tat aac ttt gac   964
Val Ala Phe Ser Thr Leu Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp
220                 225                 230                 235

aat agc cct gtg ctg cag gaa tgg gta act gcc act gac atc aga gta   1012
Asn Ser Pro Val Leu Gln Glu Trp Val Thr Ala Thr Asp Ile Arg Val
                240                 245                 250

act ctt aat cgc ctg aac act ttt gga gat gaa gtg ttt aac gat ccc   1060
Thr Leu Asn Arg Leu Asn Thr Phe Gly Asp Glu Val Phe Asn Asp Pro
            255                 260                 265

aaa gtt ctc aag tcc tat tat tat gcc atc tct gat ttt gct gta ggt   1108
Lys Val Leu Lys Ser Tyr Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly
        270                 275                 280

ggc aga tgt aaa tgt aat gga cac gca agc gag tgt atg aag aac gaa   1156
Gly Arg Cys Lys Cys Asn Gly His Ala Ser Glu Cys Met Lys Asn Glu
    285                 290                 295

ttt gat aag ctg gtg tgt aat tgc aaa cat aac aca tat gga gta gac   1204
Phe Asp Lys Leu Val Cys Asn Cys Lys His Asn Thr Tyr Gly Val Asp
300                 305                 310                 315

tgt gaa aag tgt ctt cct ttc ttc aat gac cgg ccg tgg agg agg gca   1252
Cys Glu Lys Cys Leu Pro Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala
                320                 325                 330

act gcg gaa agt gcc agt gaa tgc ctg ccc tgt gat tgc aat ggt cga   1300
Thr Ala Glu Ser Ala Ser Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg
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            335                 340                 345

tcc cag gaa tgc tac ttc gac cct gaa ctc tat cgt tcc act ggc cat   1348
Ser Gln Glu Cys Tyr Phe Asp Pro Glu Leu Tyr Arg Ser Thr Gly His
        350                 355                 360

ggg ggc cac tgt acc aac tgc cag gat aac aca gat ggc gcc cac tgt   1396
Gly Gly His Cys Thr Asn Cys Gln Asp Asn Thr Asp Gly Ala His Cys
    365                 370                 375

gag agg tgc cga gag aac ttc ttc cgc ctt ggc aac aat gaa gcc tgc   1444
Glu Arg Cys Arg Glu Asn Phe Phe Arg Leu Gly Asn Asn Glu Ala Cys
380                 385                 390                 395

tct tca tgc cac tgt agt cct gtg ggc tct cta agc aca cag tgt gat   1492
Ser Ser Cys His Cys Ser Pro Val Gly Ser Leu Ser Thr Gln Cys Asp
                400                 405                 410

agt tac ggc aga tgc agc tgt aag cca gga gtg atg ggg gac aaa tgt   1540
Ser Tyr Gly Arg Cys Ser Cys Lys Pro Gly Val Met Gly Asp Lys Cys
            415                 420                 425

gac cgt tgc cag cct gga ttc cat tct ctc act gaa gca gga tgc agg   1588
Asp Arg Cys Gln Pro Gly Phe His Ser Leu Thr Glu Ala Gly Cys Arg
        430                 435                 440

cca tgc tct tgt gat ccc tct ggc agc ata gat gaa tgt aat gtt gaa   1636
Pro Cys Ser Cys Asp Pro Ser Gly Ser Ile Asp Glu Cys Asn Val Glu
    445                 450                 455

aca gga aga tgt gtt tgc aaa gac aat gtc gaa ggc ttc aat tgt gaa   1684
Thr Gly Arg Cys Val Cys Lys Asp Asn Val Glu Gly Phe Asn Cys Glu
460                 465                 470                 475

aga tgc aaa cct gga ttt ttt aat ctg gaa tca tct aat cct cgg ggt   1732
Arg Cys Lys Pro Gly Phe Phe Asn Leu Glu Ser Ser Asn Pro Arg Gly
                480                 485                 490

tgc aca ccc tgc ttc tgc ttt ggg cat tct tct gtc tgt aca aac gct   1780
Cys Thr Pro Cys Phe Cys Phe Gly His Ser Ser Val Cys Thr Asn Ala
            495                 500                 505

gtt ggc tac agt gtt tat tct atc tcc tct acc ttt cag att gat gag   1828
Val Gly Tyr Ser Val Tyr Ser Ile Ser Ser Thr Phe Gln Ile Asp Glu
        510                 515                 520

gat ggg tgg cgt gcg gaa cag aga gat ggc tct gaa gca tct ctc gag   1876
Asp Gly Trp Arg Ala Glu Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu
    525                 530                 535

tgg tcc tct gag agg caa gat atc gcc gtg atc tca gac agc tac ttt   1924
Trp Ser Ser Glu Arg Gln Asp Ile Ala Val Ile Ser Asp Ser Tyr Phe
540                 545                 550                 555

cct cgg tac ttc att gct cct gca aag ttc ttg ggc aag cag gtg ttg   1972
Pro Arg Tyr Phe Ile Ala Pro Ala Lys Phe Leu Gly Lys Gln Val Leu
                560                 565                 570

agt tat ggt cag aac ctc tcc ttc tcc ttt cga gtg gac agg cga gat   2020
Ser Tyr Gly Gln Asn Leu Ser Phe Ser Phe Arg Val Asp Arg Arg Asp
            575                 580                 585
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act cgc ctc tct gcc gaa gac ctt gtg ctt gag gga gct ggc tta aga   2068
Thr Arg Leu Ser Ala Glu Asp Leu Val Leu Glu Gly Ala Gly Leu Arg
        590                 595                 600

gta tct gta ccc ttg atc gct cag ggc aat tcc tat cca agt gag acc   2116
Val Ser Val Pro Leu Ile Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr
    605                 610                 615

act gtg aag tat gtc ttc agg ctc cat gaa gca aca gat tac cct tgg   2164
Thr Val Lys Tyr Val Phe Arg Leu His Glu Ala Thr Asp Tyr Pro Trp
620                 625                 630                 635

agg cct gct ctt acc cct ttt gaa ttt cag aag ctc cta aac aac ttg   2212
Arg Pro Ala Leu Thr Pro Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu
                640                 645                 650

acc tct atc aag ata cgt ggg aca tac agt gag aga agt gct gga tat   2260
Thr Ser Ile Lys Ile Arg Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr
            655                 660                 665

ttg gat gat gtc acc ctg gca agt gct cgt cct ggg cct gga gtc cct   2308
Leu Asp Asp Val Thr Leu Ala Ser Ala Arg Pro Gly Pro Gly Val Pro
        670                 675                 680

gca act tgg gtg gag tcc tgc acc tgt cct gtg gga tat gga ggg cag   2356
Ala Thr Trp Val Glu Ser Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln
    685                 690                 695

ttt tgt gag atg tgc ctc tca ggt tac aga aga gaa act cct aat ctt   2404
Phe Cys Glu Met Cys Leu Ser Gly Tyr Arg Arg Glu Thr Pro Asn Leu
700                 705                 710                 715

gga cca tac agt cca tgt gtg ctt tgc gcc tgc aat gga cac agc gag   2452
Gly Pro Tyr Ser Pro Cys Val Leu Cys Ala Cys Asn Gly His Ser Glu
                720                 725                 730

acc tgt gat cct gag aca ggt gtt tgt aac tgc aga gac aat acg gct   2500
Thr Cys Asp Pro Glu Thr Gly Val Cys Asn Cys Arg Asp Asn Thr Ala
            735                 740                 745

ggc ccg cac tgt gag aag tgc agt gat ggg tac tat gga gat tca act   2548
Gly Pro His Cys Glu Lys Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr
        750                 755                 760

gca ggc acc tcc tcc gat tgc caa ccc tgt ccg tgt cct gga ggt tca   2596
Ala Gly Thr Ser Ser Asp Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser
    765                 770                 775

agt tgt gct gtt gtt ccc aag aca aag gag gtg gtg tgc acc aac tgt   2644
Ser Cys Ala Val Val Pro Lys Thr Lys Glu Val Val Cys Thr Asn Cys
780                 785                 790                 795

cct act ggc acc act ggt aag aga tgt gag ctc tgt gat gat ggc tac   2692
Pro Thr Gly Thr Thr Gly Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr
                800                 805                 810

ttt gga gac ccc ctg ggt aga aac ggc cct gtg aga ctt tgc cgc ctg   2740
Phe Gly Asp Pro Leu Gly Arg Asn Gly Pro Val Arg Leu Cys Arg Leu
            815                 820                 825
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tgc cag tgc agt gac aac atc gat ccc aac gca gtt gga aat tgc aat   2788
Cys Gln Cys Ser Asp Asn Ile Asp Pro Asn Ala Val Gly Asn Cys Asn
        830                 835                 840

cgc ttg acg gga gaa tgc ctg aag tgc atc tat aac act gct ggc ttc   2836
Arg Leu Thr Gly Glu Cys Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe
    845                 850                 855

tat tgt gac cgg tgc aaa gac gga ttt ttt gga aat ccc ctg gct ccc   2884
Tyr Cys Asp Arg Cys Lys Asp Gly Phe Phe Gly Asn Pro Leu Ala Pro
860                 865                 870                 875

aat cca gca gac aaa tgc aaa gcc tgc aat tgc aat ccg tat ggg acc   2932
Asn Pro Ala Asp Lys Cys Lys Ala Cys Asn Cys Asn Pro Tyr Gly Thr
                880                 885                 890

atg aag cag cag agc agc tgt aac ccc gtg acg ggg cag tgt gaa tgt   2980
Met Lys Gln Gln Ser Ser Cys Asn Pro Val Thr Gly Gln Cys Glu Cys
            895                 900                 905

ttg cct cac gtg act ggc cag gac tgt ggt gct tgt gac cct gga ttc   3028
Leu Pro His Val Thr Gly Gln Asp Cys Gly Ala Cys Asp Pro Gly Phe
        910                 915                 920

tac aat ctg cag agt ggg caa ggc tgt gag agg tgt gac tgc cat gcc   3076
Tyr Asn Leu Gln Ser Gly Gln Gly Cys Glu Arg Cys Asp Cys His Ala
    925                 930                 935

ttg ggc tcc acc aat ggg cag tgt gac atc cgc acc ggc cag tgt gag   3124
Leu Gly Ser Thr Asn Gly Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu
940                 945                 950                 955

tgc cag ccc ggc atc act ggt cag cac tgt gag cgc tgt gag gtc aac   3172
Cys Gln Pro Gly Ile Thr Gly Gln His Cys Glu Arg Cys Glu Val Asn
                960                 965                 970

cac ttt ggg ttt gga cct gaa ggc tgc aaa ccc tgt gac tgt cat cct   3220
His Phe Gly Phe Gly Pro Glu Gly Cys Lys Pro Cys Asp Cys His Pro
            975                 980                 985

gag gga tct ctt tca ctt cag tgc aaa gat gat ggt cgc tgt gaa tgc   3268
Glu Gly Ser Leu Ser Leu Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys
        990                 995                1000

aga gaa ggc ttt gtg gga aat cgc tgt gac cag tgt gaa gaa aac tat   3316
Arg Glu Gly Phe Val Gly Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr
   1005                1010                1015

ttc tac aat cgg tct tgg cct ggc tgc cag gaa tgt cca gct tgt tac   3364
Phe Tyr Asn Arg Ser Trp Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr
1020                1025                1030                1035

cgg ctg gta aag gat aag gtt gct gat cat aga gtg aag ctc cag gaa   3412
Arg Leu Val Lys Asp Lys Val Ala Asp His Arg Val Lys Leu Gln Glu
               1040                1045                1050

tta gag agt ctc ata gca aac ctt gga act ggg gat gag atg gtg aca   3460
Leu Glu Ser Leu Ile Ala Asn Leu Gly Thr Gly Asp Glu Met Val Thr
           1055                1060                1065

gat caa gcc ttc gag gat aga cta aag gaa gca gag agg gaa gtt atg   3508
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Asp Gln Ala Phe Glu Asp Arg Leu Lys Glu Ala Glu Arg Glu Val Met
       1070                1075                1080

gac ctc ctt cgt gag gcc cag gat gtc aaa gat gtt gac cag aat ttg   3556
Asp Leu Leu Arg Glu Ala Gln Asp Val Lys Asp Val Asp Gln Asn Leu
   1085                1090                1095

atg gat cgc cta cag aga gtg aat aac act ctg tcc agc caa att agc   3604
Met Asp Arg Leu Gln Arg Val Asn Asn Thr Leu Ser Ser Gln Ile Ser
1100                1105                1110                1115

cgt tta cag aat atc cgg aat acc att gaa gag act gga aac ttg gct   3652
Arg Leu Gln Asn Ile Arg Asn Thr Ile Glu Glu Thr Gly Asn Leu Ala
               1120                1125                1130

gaa caa gcg cgt gcc cat gta gag aac aca gag cgg ttg att gaa atc   3700
Glu Gln Ala Arg Ala His Val Glu Asn Thr Glu Arg Leu Ile Glu Ile
           1135                1140                1145

gca tcc aga gaa ctt gag aaa gca aaa gtc gct gct gcc aat gtg tca   3748
Ala Ser Arg Glu Leu Glu Lys Ala Lys Val Ala Ala Ala Asn Val Ser
       1150                1155                1160

gtc act cag cca gaa tct aca ggg gac cca aac aac atg act ctt ttg   3796
Val Thr Gln Pro Glu Ser Thr Gly Asp Pro Asn Asn Met Thr Leu Leu
   1165                1170                1175

gca gaa gag gct cga aag ctt gct gaa cgt cat aaa cag gaa gct gat   3844
Ala Glu Glu Ala Arg Lys Leu Ala Glu Arg His Lys Gln Glu Ala Asp
1180                1185                1190                1195

gac att gtt cga gtg gca aag aca gcc aat gat acg tca act gag gca   3892
Asp Ile Val Arg Val Ala Lys Thr Ala Asn Asp Thr Ser Thr Glu Ala
               1200                1205                1210

tac aac ctg ctt ctg agg aca ctg gca gga gaa aat caa aca gca ttt   3940
Tyr Asn Leu Leu Leu Arg Thr Leu Ala Gly Glu Asn Gln Thr Ala Phe
           1215                1220                1225

gag att gaa gag ctt aat agg aag tat gaa caa gcg aag aac atc tca   3988
Glu Ile Glu Glu Leu Asn Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser
       1230                1235                1240

cag gat ctg gaa aaa caa gct gcc cga gta cat gag gag gcc aaa agg   4036
Gln Asp Leu Glu Lys Gln Ala Ala Arg Val His Glu Glu Ala Lys Arg
   1245                1250                1255

gcc ggt gac aaa gct gtg gag atc tat gcc agc gtg gct cag ctg agc   4084
Ala Gly Asp Lys Ala Val Glu Ile Tyr Ala Ser Val Ala Gln Leu Ser
1260                1265                1270                1275

cct ttg gac tct gag aca ctg gag aat gaa gca aat aac ata aag atg   4132
Pro Leu Asp Ser Glu Thr Leu Glu Asn Glu Ala Asn Asn Ile Lys Met
               1280                1285                1290

gaa gct gag aat ctg gaa caa ctg att gac cag aaa tta aaa gat tat   4180
Glu Ala Glu Asn Leu Glu Gln Leu Ile Asp Gln Lys Leu Lys Asp Tyr
           1295                1300                1305

gag gac ctc aga gaa gat atg aga ggg aag gaa ctt gaa gtc aag aac   4228
Glu Asp Leu Arg Glu Asp Met Arg Gly Lys Glu Leu Glu Val Lys Asn
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ctt ctg gag aaa ggc aag act gaa cag cag acc gca gac caa ctc cta   4276
Leu Leu Glu Lys Gly Lys Thr Glu Gln Gln Thr Ala Asp Gln Leu Leu
   1325                1330                1335

gcc cga gct gat gct gcc aag gcc ctc gct gaa gaa gct gca aag aag   4324
Ala Arg Ala Asp Ala Ala Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys
1340                1345                1350                1355

gga cgg gat acc tta caa gaa gct aat gac att ctc aac aac ctg aaa   4372
Gly Arg Asp Thr Leu Gln Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys
               1360                1365                1370

gat ttt gat agg cgc gtg aac gat aac aag acg gcc gca gag gag gca   4420
Asp Phe Asp Arg Arg Val Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala
          1375                1380                1385

cta agg aag att cct gcc atc aac cag acc atc act gaa gcc aat gaa   4468
Leu Arg Lys Ile Pro Ala Ile Asn Gln Thr Ile Thr Glu Ala Asn Glu
       1390                1395                1400

aag acc aga gaa gcc cag cag gcc ctg ggc agt gct gcg gcg gat gcc   4516
Lys Thr Arg Glu Ala Gln Gln Ala Leu Gly Ser Ala Ala Ala Asp Ala
   1405                1410                1415

aca gag gcc aag aac aag gcc cat gag gcg gag agg atc gca agc gct   4564
Thr Glu Ala Lys Asn Lys Ala His Glu Ala Glu Arg Ile Ala Ser Ala
1420                1425                1430                1435

gtc caa aag aat gcc acc agc acc aag gca gaa gct gaa aga act ttt   4612
Val Gln Lys Asn Ala Thr Ser Thr Lys Ala Glu Ala Glu Arg Thr Phe
               1440                1445                1450

gca gaa gtt aca gat ctg gat aat gag gtg aac aat atg ttg aag caa   4660
Ala Glu Val Thr Asp Leu Asp Asn Glu Val Asn Asn Met Leu Lys Gln
          1455                1460                1465

ctg cag gaa gca gaa aaa gag cta aag aga aaa caa gat gac gct gac   4708
Leu Gln Glu Ala Glu Lys Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp
       1470                1475                1480

cag gac atg atg atg gca ggg atg gct tca cag gct gct caa gaa gcc   4756
Gln Asp Met Met Met Ala Gly Met Ala Ser Gln Ala Ala Gln Glu Ala
   1485                1490                1495

gag atc aat gcc aga aaa gcc aaa aac tct gtt act agc ctc ctc agc   4804
Glu Ile Asn Ala Arg Lys Ala Lys Asn Ser Val Thr Ser Leu Leu Ser
1500                1505                1510                1515

att att aat gac ctc ttg gag cag ctg ggg cag ctg gat aca gtg gac   4852
Ile Ile Asn Asp Leu Leu Glu Gln Leu Gly Gln Leu Asp Thr Val Asp
               1520                1525                1530

ctg aat aag cta aac gag att gaa ggc acc cta aac aaa gcc aaa gat   4900
Leu Asn Lys Leu Asn Glu Ile Glu Gly Thr Leu Asn Lys Ala Lys Asp
          1535                1540                1545

gaa atg aag gtc agc gat ctt gat agg aaa gtg tct gac ctg gag aat   4948
Glu Met Lys Val Ser Asp Leu Asp Arg Lys Val Ser Asp Leu Glu Asn
       1550                1555                1560
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gaa gcc aag aag cag gag gct gcc atc atg gac tat aac cga gat atc   4996
Glu Ala Lys Lys Gln Glu Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile
   1565                1570                1575

gag gag atc atg aag gac att cgc aat ctg gag gac atc agg aag acc   5044
Glu Glu Ile Met Lys Asp Ile Arg Asn Leu Glu Asp Ile Arg Lys Thr
1580                1585                1590                1595

tta cca tct ggc tgc ttc aac acc ccg tcc att gaa aag ccc gac tac   5092
Leu Pro Ser Gly Cys Phe Asn Thr Pro Ser Ile Glu Lys Pro Asp Tyr
               1600                1605                1610

aag gac gac gat gac aag tagtgtcttt agggctggaa ggcagcatcc          5140
Lys Asp Asp Asp Asp Lys
          1615

ctctgacagg ggggcagttg tgaggccaca gagtgccttg acacaaagat tacatttttc 5200

agacccccac tcctctgctg ctgtccatca ctgtcctttt gaaccaggaa aagtcacaga 5260

gtttaaagag aagcaaatta aacatcctga atcgggaaca aagggtttta tctaataaag 5320

tgtctcttcc                                                        5330
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<210> 26
<211> 1617
<212> PRT
<213> Homo sapiens

<400> 26

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Met Arg Gly Ser His Arg Ala Ala Pro Ala Leu Arg Pro Arg Gly Arg
  1               5                  10                  15

Leu Trp Pro Val Leu Ala Val Leu Ala Ala Ala Ala Ala Ala Gly Cys
            20                  25                  30

Ala Gln Ala Ala Met Asp Glu Cys Thr Asp Glu Gly Gly Arg Pro Gln
         35                  40                  45

Arg Cys Met Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val
     50                  55                  60

Ala Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr
 65                  70                  75                  80

Gly Val Thr Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln
                85                  90                  95

Pro His Leu Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln
            100                 105                 110

Ala Asp Thr Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln
        115                 120                 125

Tyr Pro Ser Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp
    130                 135                 140

Ile Thr Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe
145                 150                 155                 160
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Ala Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln
                165                 170                 175

Tyr Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly
            180                 185                 190

Phe Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu
        195                 200                 205

Phe Ser Asp Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser Thr
    210                 215                 220

Leu Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu
225                 230                 235                 240

Gln Glu Trp Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu
                245                 250                 255

Asn Thr Phe Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser
            260                 265                 270

Tyr Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys
        275                 280                 285

Asn Gly His Ala Ser Glu Cys Met Lys Asn Glu Phe Asp Lys Leu Val
    290                 295                 300

Cys Asn Cys Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu
305                 310                 315                 320

Pro Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala
                325                 330                 335

Ser Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr
            340                 345                 350

Phe Asp Pro Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr
        355                 360                 365

Asn Cys Gln Asp Asn Thr Asp Gly Ala His Cys Glu Arg Cys Arg Glu
    370                 375                 380

Asn Phe Phe Arg Leu Gly Asn Asn Glu Ala Cys Ser Ser Cys His Cys
385                 390                 395                 400

Ser Pro Val Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys
                405                 410                 415

Ser Cys Lys Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro
            420                 425                 430

Gly Phe His Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp
        435                 440                 445

Pro Ser Gly Ser Ile Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val
    450                 455                 460

Cys Lys Asp Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly
465                 470                 475                 480
```

```
Phe Phe Asn Leu Glu Ser Ser Asn Pro Arg Gly Cys Thr Pro Cys Phe
                485                 490                 495

Cys Phe Gly His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val
            500                 505                 510

Tyr Ser Ile Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Ala
        515                 520                 525

Glu Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Glu Arg
    530                 535                 540

Gln Asp Ile Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile
545                 550                 555                 560

Ala Pro Ala Lys Phe Leu Gly Lys Gln Val Leu Ser Tyr Gly Gln Asn
                565                 570                 575

Leu Ser Phe Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala
            580                 585                 590

Glu Asp Leu Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu
        595                 600                 605

Ile Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Val
    610                 615                 620

Phe Arg Leu His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Thr
625                 630                 635                 640

Pro Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile
                645                 650                 655

Arg Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr
            660                 665                 670

Leu Ala Ser Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu
        675                 680                 685

Ser Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Met Cys
    690                 695                 700

Leu Ser Gly Tyr Arg Arg Glu Thr Pro Asn Leu Gly Pro Tyr Ser Pro
705                 710                 715                 720

Cys Val Leu Cys Ala Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu
                725                 730                 735

Thr Gly Val Cys Asn Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu
            740                 745                 750

Lys Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr Ala Gly Thr Ser Ser
        755                 760                 765

Asp Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Val Val
    770                 775                 780

Pro Lys Thr Lys Glu Val Val Cys Thr Asn Cys Pro Thr Gly Thr Thr
785                 790                 795                 800

Gly Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu
```

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                805                 810                 815

Gly Arg Asn Gly Pro Val Arg Leu Cys Arg Leu Cys Gln Cys Ser Asp
            820                 825                 830

Asn Ile Asp Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu
        835                 840                 845

Cys Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys
    850                 855                 860

Lys Asp Gly Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys
865                 870                 875                 880

Cys Lys Ala Cys Asn Cys Asn Pro Tyr Gly Thr Met Lys Gln Gln Ser
                885                 890                 895

Ser Cys Asn Pro Val Thr Gly Gln Cys Glu Cys Leu Pro His Val Thr
            900                 905                 910

Gly Gln Asp Cys Gly Ala Cys Asp Pro Gly Phe Tyr Asn Leu Gln Ser
        915                 920                 925

Gly Gln Gly Cys Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn
    930                 935                 940

Gly Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile
945                 950                 955                 960

Thr Gly Gln His Cys Glu Arg Cys Glu Val Asn His Phe Gly Phe Gly
                965                 970                 975

Pro Glu Gly Cys Lys Pro Cys Asp Cys His Pro Glu Gly Ser Leu Ser
            980                 985                 990

Leu Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val
        995                1000                1005

Gly Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser
   1010                1015                1020

Trp Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp
025                1030                1035                1040

Lys Val Ala Asp His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile
               1045                1050                1055

Ala Asn Leu Gly Thr Gly Asp Glu Met Val Thr Asp Gln Ala Phe Glu
           1060                1065                1070

Asp Arg Leu Lys Glu Ala Glu Arg Glu Val Met Asp Leu Leu Arg Glu
       1075                1080                1085

Ala Gln Asp Val Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln
   1090                1095                1100

Arg Val Asn Asn Thr Leu Ser Ser Gln Ile Ser Arg Leu Gln Asn Ile
105                1110                1115                1120

Arg Asn Thr Ile Glu Glu Thr Gly Asn Leu Ala Glu Gln Ala Arg Ala
               1125                1130                1135
```

```
His Val Glu Asn Thr Glu Arg Leu Ile Glu Ile Ala Ser Arg Glu Leu
          1140                1145                1150

Glu Lys Ala Lys Val Ala Ala Ala Asn Val Ser Val Thr Gln Pro Glu
       1155                1160                1165

Ser Thr Gly Asp Pro Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg
   1170                1175                1180

Lys Leu Ala Glu Arg His Lys Gln Glu Ala Asp Asp Ile Val Arg Val
185                1190                1195                1200

Ala Lys Thr Ala Asn Asp Thr Ser Thr Glu Ala Tyr Asn Leu Leu Leu
               1205                1210                1215

Arg Thr Leu Ala Gly Glu Asn Gln Thr Ala Phe Glu Ile Glu Glu Leu
          1220                1225                1230

Asn Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys
       1235                1240                1245

Gln Ala Ala Arg Val His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala
   1250                1255                1260

Val Glu Ile Tyr Ala Ser Val Ala Gln Leu Ser Pro Leu Asp Ser Glu
265                1270                1275                1280

Thr Leu Glu Asn Glu Ala Asn Asn Ile Lys Met Glu Ala Glu Asn Leu
               1285                1290                1295

Glu Gln Leu Ile Asp Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu
          1300                1305                1310

Asp Met Arg Gly Lys Glu Leu Glu Val Lys Asn Leu Leu Glu Lys Gly
       1315                1320                1325

Lys Thr Glu Gln Gln Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala
   1330                1335                1340

Ala Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys Gly Arg Asp Thr Leu
345                1350                1355                1360

Gln Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg
               1365                1370                1375

Val Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala Leu Arg Lys Ile Pro
          1380                1385                1390

Ala Ile Asn Gln Thr Ile Thr Glu Ala Asn Glu Lys Thr Arg Glu Ala
       1395                1400                1405

Gln Gln Ala Leu Gly Ser Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn
   1410                1415                1420

Lys Ala His Glu Ala Glu Arg Ile Ala Ser Ala Val Gln Lys Asn Ala
425                1430                1435                1440

Thr Ser Thr Lys Ala Glu Ala Glu Arg Thr Phe Ala Glu Val Thr Asp
               1445                1450                1455
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Leu Asp Asn Glu Val Asn Asn Met Leu Lys Gln Leu Gln Glu Ala Glu
          1460                1465                1470

Lys Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met
       1475                1480                1485

Ala Gly Met Ala Ser Gln Ala Ala Gln Glu Ala Glu Ile Asn Ala Arg
   1490                1495                1500

Lys Ala Lys Asn Ser Val Thr Ser Leu Leu Ser Ile Ile Asn Asp Leu
505                1510                1515                1520

Leu Glu Gln Leu Gly Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn
              1525                1530                1535

Glu Ile Glu Gly Thr Leu Asn Lys Ala Lys Asp Glu Met Lys Val Ser
          1540                1545                1550

Asp Leu Asp Arg Lys Val Ser Asp Leu Glu Asn Glu Ala Lys Lys Gln
       1555                1560                1565

Glu Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile Glu Glu Ile Met Lys
   1570                1575                1580

Asp Ile Arg Asn Leu Glu Asp Ile Arg Lys Thr Leu Pro Ser Gly Cys
585                1590                1595                1600

Phe Asn Thr Pro Ser Ile Glu Lys Pro Asp Tyr Lys Asp Asp Asp Asp
              1605                1610                1615

Lys
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<210> 27
<211> 4972
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(4752)

<220>
<221> misc_feature
<222> (4729)..(4752)

<400> 27

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cag gca gcc atg gac gag tgc acg gac gag ggc ggg cgg ccg cag cgc   48
Gln Ala Ala Met Asp Glu Cys Thr Asp Glu Gly Gly Arg Pro Gln Arg
  1               5                  10                  15

tgc atg ccc gag ttc gtc aac gcc gct ttc aac gtg act gtg gtg gcc   96
Cys Met Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val Ala
             20                  25                  30

acc aac acg tgt ggg act ccg ccc gag gaa tac tgt gtg cag acc ggg   144
Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr Gly
         35                  40                  45

gtg acc ggg gtc acc aag tcc tgt cac ctg tgc gac gcc ggg cag ccc   192
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Val Thr Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln Pro
 50                  55                  60

cac ctg cag cac ggg gca gcc ttc ctg acc gac tac aac aac cag gcc   240
His Leu Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln Ala
 65                  70                  75                  80

gac acc acc tgg tgg caa agc cag acc atg ctg gcc ggg gtg cag tac   288
Asp Thr Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln Tyr
                 85                  90                  95

ccc agc tcc atc aac ctc acg ctg cac ctg gga aaa gct ttt gac atc   336
Pro Ser Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp Ile
            100                 105                 110

acc tat gtg cgt ctc aag ttc cac acc agc cgc ccg gag agc ttt gcc   384
Thr Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe Ala
        115                 120                 125

att tac aag cgc aca cgg gaa gac ggg ccc tgg att cct tac cag tac   432
Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln Tyr
    130                 135                 140

tac agt ggt tcc tgc gag aac acc tac tcc aag gca aac cgc ggc ttc   480
Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly Phe
145                 150                 155                 160

atc agg aca gga ggg gac gag cag cag gcc ttg tgt act gat gaa ttc   528
Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu Phe
                165                 170                 175

agt gac att tct ccc ctc act ggg ggc aac gtg gcc ttt tct acc ctg   576
Ser Asp Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser Thr Leu
            180                 185                 190

gaa gga agg ccc agc gcc tat aac ttt gac aat agc cct gtg ctg cag   624
Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu Gln
        195                 200                 205

gaa tgg gta act gcc act gac atc aga gta act ctt aat cgc ctg aac   672
Glu Trp Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu Asn
    210                 215                 220

act ttt gga gat gaa gtg ttt aac gat ccc aaa gtt ctc aag tcc tat   720
Thr Phe Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser Tyr
225                 230                 235                 240

tat tat gcc atc tct gat ttt gct gta ggt ggc aga tgt aaa tgt aat   768
Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys Asn
                245                 250                 255

gga cac gca agc gag tgt atg aag aac gaa ttt gat aag ctg gtg tgt   816
Gly His Ala Ser Glu Cys Met Lys Asn Glu Phe Asp Lys Leu Val Cys
            260                 265                 270

aat tgc aaa cat aac aca tat gga gta gac tgt gaa aag tgt ctt cct   864
Asn Cys Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu Pro
        275                 280                 285

ttc ttc aat gac cgg ccg tgg agg agg gca act gcg gaa agt gcc agt   912
Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala Ser
```

```
    290                 295                 300

gaa tgc ctg ccc tgt gat tgc aat ggt cga tcc cag gaa tgc tac ttc   960
Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr Phe
305                 310                 315                 320

gac cct gaa ctc tat cgt tcc act ggc cat ggg ggc cac tgt acc aac   1008
Asp Pro Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr Asn
                325                 330                 335

tgc cag gat aac aca gat ggc gcc cac tgt gag agg tgc cga gag aac   1056
Cys Gln Asp Asn Thr Asp Gly Ala His Cys Glu Arg Cys Arg Glu Asn
            340                 345                 350

ttc ttc cgc ctt ggc aac aat gaa gcc tgc tct tca tgc cac tgt agt   1104
Phe Phe Arg Leu Gly Asn Asn Glu Ala Cys Ser Ser Cys His Cys Ser
        355                 360                 365

cct gtg ggc tct cta agc aca cag tgt gat agt tac ggc aga tgc agc   1152
Pro Val Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys Ser
    370                 375                 380

tgt aag cca gga gtg atg ggg gac aaa tgt gac cgt tgc cag cct gga   1200
Cys Lys Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro Gly
385                 390                 395                 400

ttc cat tct ctc act gaa gca gga tgc agg cca tgc tct tgt gat ccc   1248
Phe His Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp Pro
                405                 410                 415

tct ggc agc ata gat gaa tgt aat gtt gaa aca gga aga tgt gtt tgc   1296
Ser Gly Ser Ile Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val Cys
            420                 425                 430

aaa gac aat gtc gaa ggc ttc aat tgt gaa aga tgc aaa cct gga ttt   1344
Lys Asp Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly Phe
        435                 440                 445

ttt aat ctg gaa tca tct aat cct cgg ggt tgc aca ccc tgc ttc tgc   1392
Phe Asn Leu Glu Ser Ser Asn Pro Arg Gly Cys Thr Pro Cys Phe Cys
    450                 455                 460

ttt ggg cat tct tct gtc tgt aca aac gct gtt ggc tac agt gtt tat   1440
Phe Gly His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val Tyr
465                 470                 475                 480

tct atc tcc tct acc ttt cag att gat gag gat ggg tgg cgt gcg gaa   1488
Ser Ile Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Ala Glu
                485                 490                 495

cag aga gat ggc tct gaa gca tct ctc gag tgg tcc tct gag agg caa   1536
Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Glu Arg Gln
            500                 505                 510

gat atc gcc gtg atc tca gac agc tac ttt cct cgg tac ttc att gct   1584
Asp Ile Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile Ala
        515                 520                 525

cct gca aag ttc ttg ggc aag cag gtg ttg agt tat ggt cag aac ctc   1632
Pro Ala Lys Phe Leu Gly Lys Gln Val Leu Ser Tyr Gly Gln Asn Leu
    530                 535                 540
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tcc ttc tcc ttt cga gtg gac agg cga gat act cgc ctc tct gcc gaa   1680
Ser Phe Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala Glu
545                 550                 555                 560

gac ctt gtg ctt gag gga gct ggc tta aga gta tct gta ccc ttg atc   1728
Asp Leu Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu Ile
                565                 570                 575

gct cag ggc aat tcc tat cca agt gag acc act gtg aag tat gtc ttc   1776
Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Val Phe
            580                 585                 590

agg ctc cat gaa gca aca gat tac cct tgg agg cct gct ctt acc cct   1824
Arg Leu His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Thr Pro
        595                 600                 605

ttt gaa ttt cag aag ctc cta aac aac ttg acc tct atc aag ata cgt   1872
Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile Arg
    610                 615                 620

ggg aca tac agt gag aga agt gct gga tat ttg gat gat gtc acc ctg   1920
Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr Leu
625                 630                 635                 640

gca agt gct cgt cct ggg cct gga gtc cct gca act tgg gtg gag tcc   1968
Ala Ser Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu Ser
                645                 650                 655

tgc acc tgt cct gtg gga tat gga ggg cag ttt tgt gag atg tgc ctc   2016
Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Met Cys Leu
            660                 665                 670

tca ggt tac aga aga gaa act cct aat ctt gga cca tac agt cca tgt   2064
Ser Gly Tyr Arg Arg Glu Thr Pro Asn Leu Gly Pro Tyr Ser Pro Cys
        675                 680                 685

gtg ctt tgc gcc tgc aat gga cac agc gag acc tgt gat cct gag aca   2112
Val Leu Cys Ala Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu Thr
    690                 695                 700

ggt gtt tgt aac tgc aga gac aat acg gct ggc ccg cac tgt gag aag   2160
Gly Val Cys Asn Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu Lys
705                 710                 715                 720

tgc agt gat ggg tac tat gga gat tca act gca ggc acc tcc tcc gat   2208
Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr Ala Gly Thr Ser Ser Asp
                725                 730                 735

tgc caa ccc tgt ccg tgt cct gga ggt tca agt tgt gct gtt gtt ccc   2256
Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Val Val Pro
            740                 745                 750

aag aca aag gag gtg gtg tgc acc aac tgt cct act ggc acc act ggt   2304
Lys Thr Lys Glu Val Val Cys Thr Asn Cys Pro Thr Gly Thr Thr Gly
        755                 760                 765

aag aga tgt gag ctc tgt gat gat ggc tac ttt gga gac ccc ctg ggt   2352
Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu Gly
    770                 775                 780
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aga aac ggc cct gtg aga ctt tgc cgc ctg tgc cag tgc agt gac aac   2400
Arg Asn Gly Pro Val Arg Leu Cys Arg Leu Cys Gln Cys Ser Asp Asn
785                 790                 795                 800

atc gat ccc aac gca gtt gga aat tgc aat cgc ttg acg gga gaa tgc   2448
Ile Asp Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu Cys
                805                 810                 815

ctg aag tgc atc tat aac act gct ggc ttc tat tgt gac cgg tgc aaa   2496
Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys Lys
            820                 825                 830

gac gga ttt ttt gga aat ccc ctg gct ccc aat cca gca gac aaa tgc   2544
Asp Gly Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys
        835                 840                 845

aaa gcc tgc aat tgc aat ccg tat ggg acc atg aag cag cag agc agc   2592
Lys Ala Cys Asn Cys Asn Pro Tyr Gly Thr Met Lys Gln Gln Ser Ser
    850                 855                 860

tgt aac ccc gtg acg ggg cag tgt gaa tgt ttg cct cac gtg act ggc   2640
Cys Asn Pro Val Thr Gly Gln Cys Glu Cys Leu Pro His Val Thr Gly
865                 870                 875                 880

cag gac tgt ggt gct tgt gac cct gga ttc tac aat ctg cag agt ggg   2688
Gln Asp Cys Gly Ala Cys Asp Pro Gly Phe Tyr Asn Leu Gln Ser Gly
                885                 890                 895

caa ggc tgt gag agg tgt gac tgc cat gcc ttg ggc tcc acc aat ggg   2736
Gln Gly Cys Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn Gly
            900                 905                 910

cag tgt gac atc cgc acc ggc cag tgt gag tgc cag ccc ggc atc act   2784
Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile Thr
        915                 920                 925

ggt cag cac tgt gag cgc tgt gag gtc aac cac ttt ggg ttt gga cct   2832
Gly Gln His Cys Glu Arg Cys Glu Val Asn His Phe Gly Phe Gly Pro
    930                 935                 940

gaa ggc tgc aaa ccc tgt gac tgt cat cct gag gga tct ctt tca ctt   2880
Glu Gly Cys Lys Pro Cys Asp Cys His Pro Glu Gly Ser Leu Ser Leu
945                 950                 955                 960

cag tgc aaa gat gat ggt cgc tgt gaa tgc aga gaa ggc ttt gtg gga   2928
Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val Gly
                965                 970                 975

aat cgc tgt gac cag tgt gaa gaa aac tat ttc tac aat cgg tct tgg   2976
Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser Trp
            980                 985                 990

cct ggc tgc cag gaa tgt cca gct tgt tac cgg ctg gta aag gat aag   3024
Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp Lys
        995                1000                1005

gtt gct gat cat aga gtg aag ctc cag gaa tta gag agt ctc ata gca   3072
Val Ala Asp His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile Ala
   1010                1015                1020

aac ctt gga act ggg gat gag atg gtg aca gat caa gcc ttc gag gat   3120
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Asn Leu Gly Thr Gly Asp Glu Met Val Thr Asp Gln Ala Phe Glu Asp
1025              1030                1035                1040

aga cta aag gaa gca gag agg gaa gtt atg gac ctc ctt cgt gag gcc   3168
Arg Leu Lys Glu Ala Glu Arg Glu Val Met Asp Leu Leu Arg Glu Ala
                1045                1050                1055

cag gat gtc aaa gat gtt gac cag aat ttg atg gat cgc cta cag aga   3216
Gln Asp Val Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln Arg
           1060                1065                1070

gtg aat aac act ctg tcc agc caa att agc cgt tta cag aat atc cgg   3264
Val Asn Asn Thr Leu Ser Ser Gln Ile Ser Arg Leu Gln Asn Ile Arg
       1075                1080                1085

aat acc att gaa gag act gga aac ttg gct gaa caa gcg cgt gcc cat   3312
Asn Thr Ile Glu Glu Thr Gly Asn Leu Ala Glu Gln Ala Arg Ala His
   1090                1095                1100

gta gag aac aca gag cgg ttg att gaa atc gca tcc aga gaa ctt gag   3360
Val Glu Asn Thr Glu Arg Leu Ile Glu Ile Ala Ser Arg Glu Leu Glu
1105                1110                1115                1120

aaa gca aaa gtc gct gct gcc aat gtg tca gtc act cag cca gaa tct   3408
Lys Ala Lys Val Ala Ala Ala Asn Val Ser Val Thr Gln Pro Glu Ser
                1125                1130                1135

aca ggg gac cca aac aac atg act ctt ttg gca gaa gag gct cga aag   3456
Thr Gly Asp Pro Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Lys
           1140                1145                1150

ctt gct gaa cgt cat aaa cag gaa gct gat gac att gtt cga gtg gca   3504
Leu Ala Glu Arg His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala
       1155                1160                1165

aag aca gcc aat gat acg tca act gag gca tac aac ctg ctt ctg agg   3552
Lys Thr Ala Asn Asp Thr Ser Thr Glu Ala Tyr Asn Leu Leu Leu Arg
   1170                1175                1180

aca ctg gca gga gaa aat caa aca gca ttt gag att gaa gag ctt aat   3600
Thr Leu Ala Gly Glu Asn Gln Thr Ala Phe Glu Ile Glu Glu Leu Asn
1185                1190                1195                1200

agg aag tat gaa caa gcg aag aac atc tca cag gat ctg gaa aaa caa   3648
Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln
                1205                1210                1215

gct gcc cga gta cat gag gag gcc aaa agg gcc ggt gac aaa gct gtg   3696
Ala Ala Arg Val His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val
           1220                1225                1230

gag atc tat gcc agc gtg gct cag ctg agc cct ttg gac tct gag aca   3744
Glu Ile Tyr Ala Ser Val Ala Gln Leu Ser Pro Leu Asp Ser Glu Thr
       1235                1240                1245

ctg gag aat gaa gca aat aac ata aag atg gaa gct gag aat ctg gaa   3792
Leu Glu Asn Glu Ala Asn Asn Ile Lys Met Glu Ala Glu Asn Leu Glu
   1250                1255                1260

caa ctg att gac cag aaa tta aaa gat tat gag gac ctc aga gaa gat   3840
Gln Leu Ile Asp Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp
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1265                1270                1275                1280

atg aga ggg aag gaa ctt gaa gtc aag aac ctt ctg gag aaa ggc aag   3888
Met Arg Gly Lys Glu Leu Glu Val Lys Asn Leu Leu Glu Lys Gly Lys
                1285                1290                1295

act gaa cag cag acc gca gac caa ctc cta gcc cga gct gat gct gcc   3936
Thr Glu Gln Gln Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala
            1300                1305                1310

aag gcc ctc gct gaa gaa gct gca aag aag gga cgg gat acc tta caa   3984
Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys Gly Arg Asp Thr Leu Gln
        1315                1320                1325

gaa gct aat gac att ctc aac aac ctg aaa gat ttt gat agg cgc gtg   4032
Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val
    1330                1335                1340

aac gat aac aag acg gcc gca gag gag gca cta agg aag att cct gcc   4080
Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala Leu Arg Lys Ile Pro Ala
1345                1350                1355                1360

atc aac cag acc atc act gaa gcc aat gaa aag acc aga gaa gcc cag   4128
Ile Asn Gln Thr Ile Thr Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln
                1365                1370                1375

cag gcc ctg ggc agt gct gcg gcg gat gcc aca gag gcc aag aac aag   4176
Gln Ala Leu Gly Ser Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys
            1380                1385                1390

gcc cat gag gcg gag agg atc gca agc gct gtc caa aag aat gcc acc   4224
Ala His Glu Ala Glu Arg Ile Ala Ser Ala Val Gln Lys Asn Ala Thr
        1395                1400                1405

agc acc aag gca gaa gct gaa aga act ttt gca gaa gtt aca gat ctg   4272
Ser Thr Lys Ala Glu Ala Glu Arg Thr Phe Ala Glu Val Thr Asp Leu
    1410                1415                1420

gat aat gag gtg aac aat atg ttg aag caa ctg cag gaa gca gaa aaa   4320
Asp Asn Glu Val Asn Asn Met Leu Lys Gln Leu Gln Glu Ala Glu Lys
1425                1430                1435                1440

gag cta aag aga aaa caa gat gac gct gac cag gac atg atg atg gca   4368
Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala
                1445                1450                1455

ggg atg gct tca cag gct gct caa gaa gcc gag atc aat gcc aga aaa   4416
Gly Met Ala Ser Gln Ala Ala Gln Glu Ala Glu Ile Asn Ala Arg Lys
            1460                1465                1470

gcc aaa aac tct gtt act agc ctc ctc agc att att aat gac ctc ttg   4464
Ala Lys Asn Ser Val Thr Ser Leu Leu Ser Ile Ile Asn Asp Leu Leu
        1475                1480                1485

gag cag ctg ggg cag ctg gat aca gtg gac ctg aat aag cta aac gag   4512
Glu Gln Leu Gly Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu
    1490                1495                1500

att gaa ggc acc cta aac aaa gcc aaa gat gaa atg aag gtc agc gat   4560
Ile Glu Gly Thr Leu Asn Lys Ala Lys Asp Glu Met Lys Val Ser Asp
1505                1510                1515                1520
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ctt gat agg aaa gtg tct gac ctg gag aat gaa gcc aag aag cag gag   4608
Leu Asp Arg Lys Val Ser Asp Leu Glu Asn Glu Ala Lys Lys Gln Glu
                1525                1530                1535

gct gcc atc atg gac tat aac cga gat atc gag gag atc atg aag gac   4656
Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile Glu Glu Ile Met Lys Asp
            1540                1545                1550

att cgc aat ctg gag gac atc agg aag acc tta cca tct ggc tgc ttc   4704
Ile Arg Asn Leu Glu Asp Ile Arg Lys Thr Leu Pro Ser Gly Cys Phe
        1555                1560                1565

aac acc ccg tcc att gaa aag ccc gac tac aag gac gac gat gac aag   4752
Asn Thr Pro Ser Ile Glu Lys Pro Asp Tyr Lys Asp Asp Asp Asp Lys
    1570                1575                1580

tagtgtcttt agggctggaa ggcagcatcc ctctgacagg ggggcagttg tgaggccaca 4812

gagtgccttg acacaaagat tacatttttc agacccccac tcctctgctg ctgtccatca 4872

ctgtcctttt gaaccaggaa aagtcacaga gtttaaagag aagcaaatta aacatcctga 4932

atcgggaaca aagggtttta tctaataaag tgtctcttcc                       4972
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Gln Ala Ala Met Asp Glu Cys Thr Asp Glu Gly Gly Arg Pro Gln Arg
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Cys Met Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val Ala
             20                  25                  30

Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr Gly
         35                  40                  45

Val Thr Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln Pro
     50                  55                  60

His Leu Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln Ala
 65                  70                  75                  80

Asp Thr Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln Tyr
                 85                  90                  95

Pro Ser Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp Ile
            100                 105                 110

Thr Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe Ala
        115                 120                 125

Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln Tyr
    130                 135                 140

Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly Phe
145                 150                 155                 160
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Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu Phe
                165                 170                 175

Ser Asp Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser Thr Leu
            180                 185                 190

Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu Gln
        195                 200                 205

Glu Trp Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu Asn
    210                 215                 220

Thr Phe Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser Tyr
225                 230                 235                 240

Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys Asn
                245                 250                 255

Gly His Ala Ser Glu Cys Met Lys Asn Glu Phe Asp Lys Leu Val Cys
            260                 265                 270

Asn Cys Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu Pro
        275                 280                 285

Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala Ser
    290                 295                 300

Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr Phe
305                 310                 315                 320

Asp Pro Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr Asn
                325                 330                 335

Cys Gln Asp Asn Thr Asp Gly Ala His Cys Glu Arg Cys Arg Glu Asn
            340                 345                 350

Phe Phe Arg Leu Gly Asn Asn Glu Ala Cys Ser Ser Cys His Cys Ser
        355                 360                 365

Pro Val Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys Ser
    370                 375                 380

Cys Lys Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro Gly
385                 390                 395                 400

Phe His Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp Pro
                405                 410                 415

Ser Gly Ser Ile Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val Cys
            420                 425                 430

Lys Asp Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly Phe
        435                 440                 445

Phe Asn Leu Glu Ser Ser Asn Pro Arg Gly Cys Thr Pro Cys Phe Cys
    450                 455                 460

Phe Gly His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val Tyr
465                 470                 475                 480
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Ser Ile Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Ala Glu
                485                 490                 495

Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Glu Arg Gln
            500                 505                 510

Asp Ile Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile Ala
        515                 520                 525

Pro Ala Lys Phe Leu Gly Lys Gln Val Leu Ser Tyr Gly Gln Asn Leu
    530                 535                 540

Ser Phe Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala Glu
545                 550                 555                 560

Asp Leu Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu Ile
                565                 570                 575

Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Val Phe
            580                 585                 590

Arg Leu His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Thr Pro
        595                 600                 605

Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile Arg
    610                 615                 620

Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr Leu
625                 630                 635                 640

Ala Ser Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu Ser
                645                 650                 655

Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Met Cys Leu
            660                 665                 670

Ser Gly Tyr Arg Arg Glu Thr Pro Asn Leu Gly Pro Tyr Ser Pro Cys
        675                 680                 685

Val Leu Cys Ala Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu Thr
    690                 695                 700

Gly Val Cys Asn Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu Lys
705                 710                 715                 720

Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr Ala Gly Thr Ser Ser Asp
                725                 730                 735

Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Val Val Pro
            740                 745                 750

Lys Thr Lys Glu Val Val Cys Thr Asn Cys Pro Thr Gly Thr Thr Gly
        755                 760                 765

Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu Gly
    770                 775                 780

Arg Asn Gly Pro Val Arg Leu Cys Arg Leu Cys Gln Cys Ser Asp Asn
785                 790                 795                 800

Ile Asp Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu Cys
```

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                805                 810                 815

Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys Lys
            820                 825                 830

Asp Gly Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys
        835                 840                 845

Lys Ala Cys Asn Cys Asn Pro Tyr Gly Thr Met Lys Gln Gln Ser Ser
    850                 855                 860

Cys Asn Pro Val Thr Gly Gln Cys Glu Cys Leu Pro His Val Thr Gly
865                 870                 875                 880

Gln Asp Cys Gly Ala Cys Asp Pro Gly Phe Tyr Asn Leu Gln Ser Gly
                885                 890                 895

Gln Gly Cys Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn Gly
            900                 905                 910

Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile Thr
        915                 920                 925

Gly Gln His Cys Glu Arg Cys Glu Val Asn His Phe Gly Phe Gly Pro
    930                 935                 940

Glu Gly Cys Lys Pro Cys Asp Cys His Pro Glu Gly Ser Leu Ser Leu
945                 950                 955                 960

Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val Gly
                965                 970                 975

Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser Trp
            980                 985                 990

Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp Lys
        995                1000                1005

Val Ala Asp His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile Ala
   1010                1015                1020

Asn Leu Gly Thr Gly Asp Glu Met Val Thr Asp Gln Ala Phe Glu Asp
1025                1030                1035                1040

Arg Leu Lys Glu Ala Glu Arg Glu Val Met Asp Leu Leu Arg Glu Ala
                1045                1050                1055

Gln Asp Val Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln Arg
           1060                1065                1070

Val Asn Asn Thr Leu Ser Ser Gln Ile Ser Arg Leu Gln Asn Ile Arg
       1075                1080                1085

Asn Thr Ile Glu Glu Thr Gly Asn Leu Ala Glu Gln Ala Arg Ala His
   1090                1095                1100

Val Glu Asn Thr Glu Arg Leu Ile Glu Ile Ala Ser Arg Glu Leu Glu
1105                1110                1115                1120

Lys Ala Lys Val Ala Ala Ala Asn Val Ser Val Thr Gln Pro Glu Ser
                1125                1130                1135
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Thr Gly Asp Pro Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Lys
          1140                1145                1150

Leu Ala Glu Arg His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala
       1155                1160                1165

Lys Thr Ala Asn Asp Thr Ser Thr Glu Ala Tyr Asn Leu Leu Leu Arg
   1170                1175                1180

Thr Leu Ala Gly Glu Asn Gln Thr Ala Phe Glu Ile Glu Glu Leu Asn
1185                1190                1195                1200

Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln
                1205                1210                1215

Ala Ala Arg Val His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val
          1220                1225                1230

Glu Ile Tyr Ala Ser Val Ala Gln Leu Ser Pro Leu Asp Ser Glu Thr
       1235                1240                1245

Leu Glu Asn Glu Ala Asn Asn Ile Lys Met Glu Ala Glu Asn Leu Glu
   1250                1255                1260

Gln Leu Ile Asp Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp
1265                1270                1275                1280

Met Arg Gly Lys Glu Leu Glu Val Lys Asn Leu Leu Glu Lys Gly Lys
                1285                1290                1295

Thr Glu Gln Gln Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala
          1300                1305                1310

Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys Gly Arg Asp Thr Leu Gln
       1315                1320                1325

Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val
   1330                1335                1340

Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala Leu Arg Lys Ile Pro Ala
1345                1350                1355                1360

Ile Asn Gln Thr Ile Thr Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln
                1365                1370                1375

Gln Ala Leu Gly Ser Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys
          1380                1385                1390

Ala His Glu Ala Glu Arg Ile Ala Ser Ala Val Gln Lys Asn Ala Thr
       1395                1400                1405

Ser Thr Lys Ala Glu Ala Glu Arg Thr Phe Ala Glu Val Thr Asp Leu
   1410                1415                1420

Asp Asn Glu Val Asn Asn Met Leu Lys Gln Leu Gln Glu Ala Glu Lys
1425                1430                1435                1440

Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala
                1445                1450                1455
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Gly Met Ala Ser Gln Ala Ala Gln Glu Ala Glu Ile Asn Ala Arg Lys
          1460                1465                1470

Ala Lys Asn Ser Val Thr Ser Leu Leu Ser Ile Ile Asn Asp Leu Leu
       1475                1480                1485

Glu Gln Leu Gly Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu
   1490                1495                1500

Ile Glu Gly Thr Leu Asn Lys Ala Lys Asp Glu Met Lys Val Ser Asp
1505                1510                1515                1520

Leu Asp Arg Lys Val Ser Asp Leu Glu Asn Glu Ala Lys Lys Gln Glu
               1525                1530                1535

Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile Glu Glu Ile Met Lys Asp
          1540                1545                1550

Ile Arg Asn Leu Glu Asp Ile Arg Lys Thr Leu Pro Ser Gly Cys Phe
       1555                1560                1565

Asn Thr Pro Ser Ile Glu Lys Pro Asp Tyr Lys Asp Asp Asp Asp Lys
   1570                1575                1580


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cgtccggctc tcggcctcca gcccggtcca cagcccggcc tcggcccgca gcggaggatc 120

ggcctcggga tacgccgcta ggcgagtgca gcgcggcacc ccagcctttg ccgaggggcc 180

cgccgcagcg gg atg acg ggc ggc ggg cgg gcc gcg ctg gcc ctg cag ccc 231
              Met Thr Gly Gly Gly Arg Ala Ala Leu Ala Leu Gln Pro
                1               5                   10

cgg ggg cgg ctg tgg ccg ctg ttg gct gtg ctg gcg gct gtg gcg ggc   279
Arg Gly Arg Leu Trp Pro Leu Leu Ala Val Leu Ala Ala Val Ala Gly
     15                  20                  25

tgt gtc cgg gcg gcc atg gac gag tgc gcg gat gag ggc ggg cgg ccg   327
Cys Val Arg Ala Ala Met Asp Glu Cys Ala Asp Glu Gly Gly Arg Pro
 30                  35                  40                  45

cag cgc tgc atg ccg gag ttt gtt aat gcc gcc ttc aat gtg acc gtg   375
Gln Arg Cys Met Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val
                 50                  55                  60
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gtg gct acc aac acg tgt ggg act ccg ccc gag gag tac tgc gtg cag   423
Val Ala Thr Asn Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln
            65                  70                  75

act ggg gtg acc gga gtc act aag tcc tgt cac ctg tgc gac gcc ggc   471
Thr Gly Val Thr Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly
        80                  85                  90

cag cag cac ctg caa cac ggg gca gcc ttc ctg acc gac tac aac aac   519
Gln Gln His Leu Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn
    95                  100                 105

cag gcc gac acc acc tgg tgg caa agc cag act atg ctg gcc ggg gtg   567
Gln Ala Asp Thr Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val
110                 115                 120                 125

cag tac ccc aac tcc atc aac ctc acg ctg cac ctg gga aag gct ttt   615
Gln Tyr Pro Asn Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe
                130                 135                 140

gac atc act tac gtg cgc ctc aag ttc cac acc agc cgt cca gag agc   663
Asp Ile Thr Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser
            145                 150                 155

ttc gcc atc tat aag cgc act cgg gaa gac ggg ccc tgg att cct tat   711
Phe Ala Ile Tyr Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr
        160                 165                 170

cag tac tac agt ggg tcc tgt gag aac acg tac tca aag gct aac cgt   759
Gln Tyr Tyr Ser Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg
    175                 180                 185

ggc ttc atc agg acc gga ggg gac gag cag cag gcc ttg tgt act gat   807
Gly Phe Ile Arg Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp
190                 195                 200                 205

gaa ttc agt gac att tcc ccc ctc acc ggt ggc aac gtg gcc ttt tca   855
Glu Phe Ser Asp Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser
                210                 215                 220

acc ctg gaa gga cgg ccg agt gcc tac aac ttt gac aac agc cct gtg   903
Thr Leu Glu Gly Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val
            225                 230                 235

ctc cag gaa tgg gta act gcc act gac atc aga gtg acg ctc aat cgc   951
Leu Gln Glu Trp Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg
        240                 245                 250

ctg aac acc ttt gga gat gaa gtg ttt aac gac ccc aaa gtt ctc aag   999
Leu Asn Thr Phe Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys
    255                 260                 265

tct tac tat tac gca atc tca gac ttt gct gtg ggc ggc agg tgt aaa   1047
Ser Tyr Tyr Tyr Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys
270                 275                 280                 285

tgt aac gga cat gcc agc gag tgt gta aag aac gag ttt gac aaa ctc   1095
Cys Asn Gly His Ala Ser Glu Cys Val Lys Asn Glu Phe Asp Lys Leu
                290                 295                 300

atg tgc aac tgc aaa cat aac aca tac gga gtt gac tgt gaa aag tgc   1143
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Met Cys Asn Cys Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys
            305                 310                 315

ctg cct ttc ttc aat gac cgg ccg tgg agg agg gcg act gct gag agc   1191
Leu Pro Phe Phe Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser
        320                 325                 330

gcc agc gag tgc ctt cct tgt gac tgc aat ggc cga tcc caa gag tgc   1239
Ala Ser Glu Cys Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys
    335                 340                 345

tac ttt gat cct gaa cta tac cgt tcc act gga cat ggt ggc cac tgt   1287
Tyr Phe Asp Pro Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys
350                 355                 360                 365

acc aac tgc cgg gat aac aca gat ggt gcc aag tgc gag agg tgc cgg   1335
Thr Asn Cys Arg Asp Asn Thr Asp Gly Ala Lys Cys Glu Arg Cys Arg
                370                 375                 380

gag aat ttc ttc cgc ctg ggg aac act gaa gcc tgc tct ccg tgc cac   1383
Glu Asn Phe Phe Arg Leu Gly Asn Thr Glu Ala Cys Ser Pro Cys His
            385                 390                 395

tgc agc cct gtt ggt tct ctc agc aca cag tgt gac agt tac ggc aga   1431
Cys Ser Pro Val Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg
        400                 405                 410

tgc agc tgt aag cca gga gtg atg ggt gac aag tgt gac cgt tgt cag   1479
Cys Ser Cys Lys Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln
    415                 420                 425

cct ggg ttc cat tcc ctc act gag gca gga tgc agg cca tgc tcc tgc   1527
Pro Gly Phe His Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys
430                 435                 440                 445

gat cct tcg ggc agc aca gac gag tgt aat gtt gaa aca gga aga tgc   1575
Asp Pro Ser Gly Ser Thr Asp Glu Cys Asn Val Glu Thr Gly Arg Cys
                450                 455                 460

gtt tgc aaa gac aat gtt gaa ggc ttc aac tgt gag aga tgc aaa cct   1623
Val Cys Lys Asp Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro
            465                 470                 475

gga ttt ttt aat ctg gag tca tct aat cct aag ggc tgc aca ccc tgc   1671
Gly Phe Phe Asn Leu Glu Ser Ser Asn Pro Lys Gly Cys Thr Pro Cys
        480                 485                 490

ttc tgc ttt ggc cat tct tct gtg tgc aca aat gct gtt ggc tac agt   1719
Phe Cys Phe Gly His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser
    495                 500                 505

gtt tat gac atc tcc tcc acc ttt cag att gat gag gat ggg tgg cgc   1767
Val Tyr Asp Ile Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg
510                 515                 520                 525

gtg gag cag aga gat ggc tcg gag gcg tct ctg gag tgg tcc tca gac   1815
Val Glu Gln Arg Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Asp
                530                 535                 540

agg caa tat att gcc gta atc tca gac agt tac ttt cct aga tac ttc   1863
Arg Gln Tyr Ile Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe
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            545                 550                 555

atc gcc cct gtg aag ttc ctg ggc aac cag gtc ctg agt tat ggg cag   1911
Ile Ala Pro Val Lys Phe Leu Gly Asn Gln Val Leu Ser Tyr Gly Gln
        560                 565                 570

aat ctt tcc ttc tcc ttc cga gtg gac aga cga gac act cgc ctc tcc   1959
Asn Leu Ser Phe Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser
    575                 580                 585

gca gag gac ctt gtg ctc gaa gga gct ggc ttg aga gta tcc gtg ccc   2007
Ala Glu Asp Leu Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro
590                 595                 600                 605

ttg atc gct cag ggc aac tcc tac ccc agc gag acc act gtg aag tac   2055
Leu Ile Ala Gln Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr
                610                 615                 620

atc ttc agg ctc cat gaa gca acg gat tac cct tgg agg ccc gct ctc   2103
Ile Phe Arg Leu His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu
            625                 630                 635

tcc ccg ttt gaa ttt cag aag ctc ctg aac aac ttg acc tct atc aag   2151
Ser Pro Phe Glu Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys
        640                 645                 650

atc cgt ggt aca tac agc gag agg agc gct ggg tac ttg gat gat gtc   2199
Ile Arg Gly Thr Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val
    655                 660                 665

acc ttg caa agt gct cgc cct ggg ccc gga gtc cct gca acg tgg gtg   2247
Thr Leu Gln Ser Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val
670                 675                 680                 685

gag tcc tgc acc tgt cca gtg gga tac ggg gga cag ttc tgt gag acg   2295
Glu Ser Cys Thr Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Thr
                690                 695                 700

tgc ctc cca ggg tac aga aga gaa act cca agc ctt gga cct tat agc   2343
Cys Leu Pro Gly Tyr Arg Arg Glu Thr Pro Ser Leu Gly Pro Tyr Ser
            705                 710                 715

ccg tgt gtg ctc tgt acc tgt aat ggg cac agt gag acc tgt gac ccg   2391
Pro Cys Val Leu Cys Thr Cys Asn Gly His Ser Glu Thr Cys Asp Pro
        720                 725                 730

gag aca ggt gtc tgt gac tgc aga gac aat aca gcc ggc ccc cac tgt   2439
Glu Thr Gly Val Cys Asp Cys Arg Asp Asn Thr Ala Gly Pro His Cys
    735                 740                 745

gag aaa tgt agc gat ggg tac tat ggg gac tca acc ctg ggc acc tcc   2487
Glu Lys Cys Ser Asp Gly Tyr Tyr Gly Asp Ser Thr Leu Gly Thr Ser
750                 755                 760                 765

tct gac tgc cag cct tgt ccc tgc ccc ggt ggc tca agt tgt gcc att   2535
Ser Asp Cys Gln Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Ile
                770                 775                 780

gtc cca aag aca aag gaa gtg gtg tgc acg cac tgt ccg act ggc act   2583
Val Pro Lys Thr Lys Glu Val Val Cys Thr His Cys Pro Thr Gly Thr
            785                 790                 795
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gcc ggc aag aga tgt gaa ctc tgt gat gac ggc tac ttt gga gac cct   2631
Ala Gly Lys Arg Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro
        800                 805                 810

ctg ggc agc aat ggg ccc gtg aga ctg tgc cgc ccg tgc cag tgt aac   2679
Leu Gly Ser Asn Gly Pro Val Arg Leu Cys Arg Pro Cys Gln Cys Asn
    815                 820                 825

gac aac ata gac ccc aac gcg gtt ggc aac tgc aac cgc ctg acg ggc   2727
Asp Asn Ile Asp Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly
830                 835                 840                 845

gag tgc ctg aag tgc atc tat aac acg gct ggt ttc tac tgc gac cgg   2775
Glu Cys Leu Lys Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg
                850                 855                 860

tgc aag gaa ggg ttt ttc gga aat ccc ctg gct ccc aat cca gcc gac   2823
Cys Lys Glu Gly Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp
            865                 870                 875

aaa tgc aaa gcc tgc gcc tgc aac tac ggg aca gtg cag caa cag agc   2871
Lys Cys Lys Ala Cys Ala Cys Asn Tyr Gly Thr Val Gln Gln Gln Ser
        880                 885                 890

agc tgt aac ccg gtg acc gga caa tgc cag tgt ctg cct cat gtg tct   2919
Ser Cys Asn Pro Val Thr Gly Gln Cys Gln Cys Leu Pro His Val Ser
    895                 900                 905

ggc cgc gac tgc ggt act tgt gac cct ggc tac tac aac ctg cag agc   2967
Gly Arg Asp Cys Gly Thr Cys Asp Pro Gly Tyr Tyr Asn Leu Gln Ser
910                 915                 920                 925

ggg caa ggc tgc gag agg tgt gac tgc cat gct ttg ggt tcc acc aat   3015
Gly Gln Gly Cys Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn
                930                 935                 940

ggg cag tgt gac atc cgc acc ggg cag tgt gag tgc cag cct ggc atc   3063
Gly Gln Cys Asp Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile
            945                 950                 955

acc ggt cag cac tgt gag cgc tgt gag acc aac cac ttt ggg ttt gga   3111
Thr Gly Gln His Cys Glu Arg Cys Glu Thr Asn His Phe Gly Phe Gly
        960                 965                 970

cct gaa ggc tgc aaa cct tgt gac tgt cac cat gaa gga tcc ctt tcg   3159
Pro Glu Gly Cys Lys Pro Cys Asp Cys His His Glu Gly Ser Leu Ser
    975                 980                 985

ctc cag tgt aaa gac gac ggc cgt tgt gaa tgc agg gaa ggc ttt gtg   3207
Leu Gln Cys Lys Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val
990                 995                1000                1005

ggc aat cgc tgt gac cag tgt gaa gag aac tat ttc tac aat cgg tcc   3255
Gly Asn Arg Cys Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser
                1010                1015                1020

tgg cct ggc tgc cag gag tgt ccg gct tgt tac cga ctt gtg aag gat   3303
Trp Pro Gly Cys Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp
            1025                1030                1035
```

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aag gct gct gag cat cga gtg aaa ctc cag gag tta gag agc ctc atc   3351
Lys Ala Ala Glu His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile
       1040                1045                1050

gcc aac ctt ggc act ggg gat gac atg gtg aca gat caa gcc ttt gag   3399
Ala Asn Leu Gly Thr Gly Asp Asp Met Val Thr Asp Gln Ala Phe Glu
   1055                1060                1065

gac aga ctt aag gaa gca gaa agg gag gtg aca gac ctt ctc cgt gag   3447
Asp Arg Leu Lys Glu Ala Glu Arg Glu Val Thr Asp Leu Leu Arg Glu
1070                1075                1080                1085

gct cag gaa gtc aaa gat gta gat caa aat ctg atg gat cgc ctt cag   3495
Ala Gln Glu Val Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln
               1090                1095                1100

aga gta aat agc agc ctg cat agc caa att agc cga ctg cag aat atc   3543
Arg Val Asn Ser Ser Leu His Ser Gln Ile Ser Arg Leu Gln Asn Ile
           1105                1110                1115

cgg aat act atc gaa gag acc ggg atc ttg gct gag cga gca cgg tcc   3591
Arg Asn Thr Ile Glu Glu Thr Gly Ile Leu Ala Glu Arg Ala Arg Ser
       1120                1125                1130

cga gtg gag agt aca gag cag ctg att gag atc gcc tcc agg gag ctc   3639
Arg Val Glu Ser Thr Glu Gln Leu Ile Glu Ile Ala Ser Arg Glu Leu
   1135                1140                1145

gag aaa gca aaa atg gcc gcc aat gtg tca atc act cag cca gag tct   3687
Glu Lys Ala Lys Met Ala Ala Asn Val Ser Ile Thr Gln Pro Glu Ser
1150                1155                1160                1165

aca ggg gag cca aac aac atg acc ctc ttg gca gaa gaa gcc cga agg   3735
Thr Gly Glu Pro Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Arg
               1170                1175                1180

ctt gca gag cgt cat aaa cag gaa gcc gat gac att gta cga gtg gca   3783
Leu Ala Glu Arg His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala
           1185                1190                1195

aag aca gcc aac gag act tca gct gag gca tat aat ctg ctt ttg agg   3831
Lys Thr Ala Asn Glu Thr Ser Ala Glu Ala Tyr Asn Leu Leu Leu Arg
       1200                1205                1210

acc ctg gca gga gaa aat caa act gcg ctg gag att gaa gaa ctt aac   3879
Thr Leu Ala Gly Glu Asn Gln Thr Ala Leu Glu Ile Glu Glu Leu Asn
   1215                1220                1225

cgg aag tac gaa caa gca aag aac atc tct cag gac ctg gag aag cag   3927
Arg Lys Tyr Glu Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln
1230                1235                1240                1245

gct gcc cga gtc cat gag gaa gcc aag cgt gca ggt gac aaa gcc gta   3975
Ala Ala Arg Val His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val
               1250                1255                1260

gag atc tat gcc agt gtg gcc cag ctg acc cct gtg gac tct gag gcc   4023
Glu Ile Tyr Ala Ser Val Ala Gln Leu Thr Pro Val Asp Ser Glu Ala
           1265                1270                1275

ctg gag aat gaa gca aat aaa atc aag aaa gaa gct gca gac ctg gac   4071
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Leu Glu Asn Glu Ala Asn Lys Ile Lys Lys Glu Ala Ala Asp Leu Asp
       1280                1285                1290

cgt ctg att gac cag aag cta aag gat tac gag gac ctc agg gaa gac   4119
Arg Leu Ile Asp Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp
   1295                1300                1305

atg aga gga aag gaa cat gaa gtg aag aac ctt cta gag aag ggg aaa   4167
Met Arg Gly Lys Glu His Glu Val Lys Asn Leu Leu Glu Lys Gly Lys
1310                1315                1320                1325

gct gaa cag cag acc gcc gac caa ctc cta gct cga gcc gat gct gcc   4215
Ala Glu Gln Gln Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala
               1330                1335                1340

aag gcc ctt gct gaa gaa gct gct aag aag gga cgc agt acc tta caa   4263
Lys Ala Leu Ala Glu Glu Ala Ala Lys Lys Gly Arg Ser Thr Leu Gln
           1345                1350                1355

gaa gcc aat gac att ctc aac aac ctg aaa gat ttt gat aga cgt gtg   4311
Glu Ala Asn Asp Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val
       1360                1365                1370

aac gat aac aag aca gcc gcg gaa gaa gct cta agg aga att ccc gcc   4359
Asn Asp Asn Lys Thr Ala Ala Glu Glu Ala Leu Arg Arg Ile Pro Ala
   1375                1380                1385

atc aac cgg acc ata gct gaa gcc aat gag aag aca agg gag gcc cag   4407
Ile Asn Arg Thr Ile Ala Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln
1390                1395                1400                1405

cta gcg ctg ggc aat gct gcc gct gac gcc acg gag gcc aag aac aag   4455
Leu Ala Leu Gly Asn Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys
               1410                1415                1420

gcc cat gag gca gag agg atc gcc agc gcc gcg cag aag aat gcc acc   4503
Ala His Glu Ala Glu Arg Ile Ala Ser Ala Ala Gln Lys Asn Ala Thr
           1425                1430                1435

agt acc aag gcg gac gca gaa aga acc ttc ggg gaa gtt aca gat ctg   4551
Ser Thr Lys Ala Asp Ala Glu Arg Thr Phe Gly Glu Val Thr Asp Leu
       1440                1445                1450

gat aat gag gtg aac ggt atg ctg agg cag cta gag gag gca gag aat   4599
Asp Asn Glu Val Asn Gly Met Leu Arg Gln Leu Glu Glu Ala Glu Asn
   1455                1460                1465

gag ctg aag agg aag caa gat gac gcc gac cag gac atg atg atg gcg   4647
Glu Leu Lys Arg Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala
1470                1475                1480                1485

ggg atg gct tcg caa gcc gct cag gag gct gag ctc aat gcc aga aag   4695
Gly Met Ala Ser Gln Ala Ala Gln Glu Ala Glu Leu Asn Ala Arg Lys
               1490                1495                1500

gcc aaa aac tct gtc agc agc ctc ctc agc cag ctg aac aac ctc ttg   4743
Ala Lys Asn Ser Val Ser Ser Leu Leu Ser Gln Leu Asn Asn Leu Leu
           1505                1510                1515

gat cag cta gga cag ctg gac aca gtg gac ctg aac aag ctc aat gag   4791
Asp Gln Leu Gly Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu
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      1520                1525                1530

atc gaa ggc tcc ctg aac aaa gcc aaa gac gaa atg aag gcc agc gac   4839
Ile Glu Gly Ser Leu Asn Lys Ala Lys Asp Glu Met Lys Ala Ser Asp
   1535                1540                1545

ctg gac agg aag gtg tct gac ctg gag agc gag gct cgg aag cag gaa   4887
Leu Asp Arg Lys Val Ser Asp Leu Glu Ser Glu Ala Arg Lys Gln Glu
1550                1555                1560                1565

gca gcc atc atg gac tat aac cgg gac ata gca gag atc att aag gat   4935
Ala Ala Ile Met Asp Tyr Asn Arg Asp Ile Ala Glu Ile Ile Lys Asp
               1570                1575                1580

att cac aac ctg gag gac atc aag aag acc cta cca acc ggc tgc ttc   4983
Ile His Asn Leu Glu Asp Ile Lys Lys Thr Leu Pro Thr Gly Cys Phe
          1585                1590                1595

aac acc ccg tct atc gag aag ccc tag tggcgagagg gctgtaaggc         5030
Asn Thr Pro Ser Ile Glu Lys Pro
      1600                1605

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cttt 7554

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<212> PRT
<213> Mus musculus

<400> 30
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Leu Trp Pro Leu Leu Ala Val Leu Ala Ala Val Ala Gly Cys Val Arg
20 25 30

Ala Ala Met Asp Glu Cys Ala Asp Glu Gly Gly Arg Pro Gln Arg Cys

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        35                  40                  45

Met Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val Ala Thr
     50                  55                  60

Asn Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr Gly Val
 65                  70                  75                  80

Thr Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln Gln His
                 85                  90                  95

Leu Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln Ala Asp
            100                 105                 110

Thr Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln Tyr Pro
        115                 120                 125

Asn Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp Ile Thr
    130                 135                 140

Tyr Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe Ala Ile
145                 150                 155                 160

Tyr Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln Tyr Tyr
                165                 170                 175

Ser Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly Phe Ile
            180                 185                 190

Arg Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu Phe Ser
        195                 200                 205

Asp Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser Thr Leu Glu
    210                 215                 220

Gly Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu Gln Glu
225                 230                 235                 240

Trp Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu Asn Thr
                245                 250                 255

Phe Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser Tyr Tyr
            260                 265                 270

Tyr Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys Asn Gly
        275                 280                 285

His Ala Ser Glu Cys Val Lys Asn Glu Phe Asp Lys Leu Met Cys Asn
    290                 295                 300

Cys Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu Pro Phe
305                 310                 315                 320

Phe Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala Ser Glu
                325                 330                 335

Cys Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr Phe Asp
            340                 345                 350

Pro Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr Asn Cys
        355                 360                 365
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Arg Asp Asn Thr Asp Gly Ala Lys Cys Glu Arg Cys Arg Glu Asn Phe
    370                 375                 380

Phe Arg Leu Gly Asn Thr Glu Ala Cys Ser Pro Cys His Cys Ser Pro
385                 390                 395                 400

Val Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys Ser Cys
                405                 410                 415

Lys Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro Gly Phe
            420                 425                 430

His Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp Pro Ser
        435                 440                 445

Gly Ser Thr Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val Cys Lys
    450                 455                 460

Asp Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly Phe Phe
465                 470                 475                 480

Asn Leu Glu Ser Ser Asn Pro Lys Gly Cys Thr Pro Cys Phe Cys Phe
                485                 490                 495

Gly His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val Tyr Asp
            500                 505                 510

Ile Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Val Glu Gln
        515                 520                 525

Arg Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Asp Arg Gln Tyr
    530                 535                 540

Ile Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile Ala Pro
545                 550                 555                 560

Val Lys Phe Leu Gly Asn Gln Val Leu Ser Tyr Gly Gln Asn Leu Ser
                565                 570                 575

Phe Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala Glu Asp
            580                 585                 590

Leu Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu Ile Ala
        595                 600                 605

Gln Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Ile Phe Arg
    610                 615                 620

Leu His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Ser Pro Phe
625                 630                 635                 640

Glu Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile Arg Gly
                645                 650                 655

Thr Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr Leu Gln
            660                 665                 670

Ser Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu Ser Cys
        675                 680                 685
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Thr Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Thr Cys Leu Pro
    690                 695                 700

Gly Tyr Arg Arg Glu Thr Pro Ser Leu Gly Pro Tyr Ser Pro Cys Val
705                 710                 715                 720

Leu Cys Thr Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu Thr Gly
                725                 730                 735

Val Cys Asp Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu Lys Cys
            740                 745                 750

Ser Asp Gly Tyr Tyr Gly Asp Ser Thr Leu Gly Thr Ser Ser Asp Cys
        755                 760                 765

Gln Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Ile Val Pro Lys
    770                 775                 780

Thr Lys Glu Val Val Cys Thr His Cys Pro Thr Gly Thr Ala Gly Lys
785                 790                 795                 800

Arg Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu Gly Ser
                805                 810                 815

Asn Gly Pro Val Arg Leu Cys Arg Pro Cys Gln Cys Asn Asp Asn Ile
            820                 825                 830

Asp Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu Cys Leu
        835                 840                 845

Lys Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys Lys Glu
    850                 855                 860

Gly Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Lys
865                 870                 875                 880

Ala Cys Ala Cys Asn Tyr Gly Thr Val Gln Gln Gln Ser Ser Cys Asn
                885                 890                 895

Pro Val Thr Gly Gln Cys Gln Cys Leu Pro His Val Ser Gly Arg Asp
            900                 905                 910

Cys Gly Thr Cys Asp Pro Gly Tyr Tyr Asn Leu Gln Ser Gly Gln Gly
        915                 920                 925

Cys Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn Gly Gln Cys
    930                 935                 940

Asp Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile Thr Gly Gln
945                 950                 955                 960

His Cys Glu Arg Cys Glu Thr Asn His Phe Gly Phe Gly Pro Glu Gly
                965                 970                 975

Cys Lys Pro Cys Asp Cys His His Glu Gly Ser Leu Ser Leu Gln Cys
            980                 985                 990

Lys Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val Gly Asn Arg
        995                1000                1005

Cys Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser Trp Pro Gly
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   1010                1015                1020

Cys Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp Lys Ala Ala
025                1030                1035                1040

Glu His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile Ala Asn Leu
               1045                1050                1055

Gly Thr Gly Asp Asp Met Val Thr Asp Gln Ala Phe Glu Asp Arg Leu
           1060                1065                1070

Lys Glu Ala Glu Arg Glu Val Thr Asp Leu Leu Arg Glu Ala Gln Glu
       1075                1080                1085

Val Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln Arg Val Asn
   1090                1095                1100

Ser Ser Leu His Ser Gln Ile Ser Arg Leu Gln Asn Ile Arg Asn Thr
105                1110                1115                1120

Ile Glu Glu Thr Gly Ile Leu Ala Glu Arg Ala Arg Ser Arg Val Glu
               1125                1130                1135

Ser Thr Glu Gln Leu Ile Glu Ile Ala Ser Arg Glu Leu Glu Lys Ala
           1140                1145                1150

Lys Met Ala Ala Asn Val Ser Ile Thr Gln Pro Glu Ser Thr Gly Glu
       1155                1160                1165

Pro Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Arg Leu Ala Glu
   1170                1175                1180

Arg His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala Lys Thr Ala
185                1190                1195                1200

Asn Glu Thr Ser Ala Glu Ala Tyr Asn Leu Leu Leu Arg Thr Leu Ala
               1205                1210                1215

Gly Glu Asn Gln Thr Ala Leu Glu Ile Glu Glu Leu Asn Arg Lys Tyr
           1220                1225                1230

Glu Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln Ala Ala Arg
       1235                1240                1245

Val His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val Glu Ile Tyr
   1250                1255                1260

Ala Ser Val Ala Gln Leu Thr Pro Val Asp Ser Glu Ala Leu Glu Asn
265                1270                1275                1280

Glu Ala Asn Lys Ile Lys Lys Glu Ala Ala Asp Leu Asp Arg Leu Ile
               1285                1290                1295

Asp Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp Met Arg Gly
           1300                1305                1310

Lys Glu His Glu Val Lys Asn Leu Leu Glu Lys Gly Lys Ala Glu Gln
       1315                1320                1325

Gln Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala Lys Ala Leu
   1330                1335                1340
```

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Ala Glu Glu Ala Ala Lys Lys Gly Arg Ser Thr Leu Gln Glu Ala Asn
345                 1350                1355                1360

Asp Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val Asn Asp Asn
                1365                1370                1375

Lys Thr Ala Ala Glu Glu Ala Leu Arg Arg Ile Pro Ala Ile Asn Arg
            1380                1385                1390

Thr Ile Ala Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln Leu Ala Leu
        1395                1400                1405

Gly Asn Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys Ala His Glu
    1410                1415                1420

Ala Glu Arg Ile Ala Ser Ala Ala Gln Lys Asn Ala Thr Ser Thr Lys
425                 1430                1435                1440

Ala Asp Ala Glu Arg Thr Phe Gly Glu Val Thr Asp Leu Asp Asn Glu
                1445                1450                1455

Val Asn Gly Met Leu Arg Gln Leu Glu Glu Ala Glu Asn Glu Leu Lys
            1460                1465                1470

Arg Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala Gly Met Ala
        1475                1480                1485

Ser Gln Ala Ala Gln Glu Ala Glu Leu Asn Ala Arg Lys Ala Lys Asn
    1490                1495                1500

Ser Val Ser Ser Leu Leu Ser Gln Leu Asn Asn Leu Leu Asp Gln Leu
505                 1510                1515                1520

Gly Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu Ile Glu Gly
                1525                1530                1535

Ser Leu Asn Lys Ala Lys Asp Glu Met Lys Ala Ser Asp Leu Asp Arg
            1540                1545                1550

Lys Val Ser Asp Leu Glu Ser Glu Ala Arg Lys Gln Glu Ala Ala Ile
        1555                1560                1565

Met Asp Tyr Asn Arg Asp Ile Ala Glu Ile Ile Lys Asp Ile His Asn
    1570                1575                1580

Leu Glu Asp Ile Lys Lys Thr Leu Pro Thr Gly Cys Phe Asn Thr Pro
585                 1590                1595                1600

Ser Ile Glu Lys Pro
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Ala Met Asp Glu Cys Ala Asp Glu Gly Gly Arg Pro Gln Arg Cys Met
  1               5                  10                  15

ccg gag ttt gtt aat gcc gcc ttc aat gtg acc gtg gtg gct acc aac   96
Pro Glu Phe Val Asn Ala Ala Phe Asn Val Thr Val Val Ala Thr Asn
            20                  25                  30

acg tgt ggg act ccg ccc gag gag tac tgc gtg cag act ggg gtg acc   144
Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr Gly Val Thr
        35                  40                  45

gga gtc act aag tcc tgt cac ctg tgc gac gcc ggc cag cag cac ctg   192
Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln Gln His Leu
    50                  55                  60

caa cac ggg gca gcc ttc ctg acc gac tac aac aac cag gcc gac acc   240
Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln Ala Asp Thr
65                  70                  75                  80

acc tgg tgg caa agc cag act atg ctg gcc ggg gtg cag tac ccc aac   288
Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln Tyr Pro Asn
                85                  90                  95

tcc atc aac ctc acg ctg cac ctg gga aag gct ttt gac atc act tac   336
Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp Ile Thr Tyr
            100                 105                 110

gtg cgc ctc aag ttc cac acc agc cgt cca gag agc ttc gcc atc tat   384
Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe Ala Ile Tyr
        115                 120                 125

aag cgc act cgg gaa gac ggg ccc tgg att cct tat cag tac tac agt   432
Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln Tyr Tyr Ser
    130                 135                 140

ggg tcc tgt gag aac acg tac tca aag gct aac cgt ggc ttc atc agg   480
Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly Phe Ile Arg
145                 150                 155                 160

acc gga ggg gac gag cag cag gcc ttg tgt act gat gaa ttc agt gac   528
Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu Phe Ser Asp
                165                 170                 175

att tcc ccc ctc acc ggt ggc aac gtg gcc ttt tca acc ctg gaa gga   576
Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser Thr Leu Glu Gly
            180                 185                 190

cgg ccg agt gcc tac aac ttt gac aac agc cct gtg ctc cag gaa tgg   624
Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu Gln Glu Trp
        195                 200                 205

gta act gcc act gac atc aga gtg acg ctc aat cgc ctg aac acc ttt   672
Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu Asn Thr Phe
    210                 215                 220

gga gat gaa gtg ttt aac gac ccc aaa gtt ctc aag tct tac tat tac   720
Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser Tyr Tyr Tyr
225                 230                 235                 240
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gca atc tca gac ttt gct gtg ggc ggc agg tgt aaa tgt aac gga cat   768
Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys Asn Gly His
                245                 250                 255

gcc agc gag tgt gta aag aac gag ttt gac aaa ctc atg tgc aac tgc   816
Ala Ser Glu Cys Val Lys Asn Glu Phe Asp Lys Leu Met Cys Asn Cys
            260                 265                 270

aaa cat aac aca tac gga gtt gac tgt gaa aag tgc ctg cct ttc ttc   864
Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu Pro Phe Phe
        275                 280                 285

aat gac cgg ccg tgg agg agg gcg act gct gag agc gcc agc gag tgc   912
Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala Ser Glu Cys
    290                 295                 300

ctt cct tgt gac tgc aat ggc cga tcc caa gag tgc tac ttt gat cct   960
Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr Phe Asp Pro
305                 310                 315                 320

gaa cta tac cgt tcc act gga cat ggt ggc cac tgt acc aac tgc cgg   1008
Glu Leu Tyr Arg Ser Thr Gly His Gly Gly His Cys Thr Asn Cys Arg
                325                 330                 335

gat aac aca gat ggt gcc aag tgc gag agg tgc cgg gag aat ttc ttc   1056
Asp Asn Thr Asp Gly Ala Lys Cys Glu Arg Cys Arg Glu Asn Phe Phe
            340                 345                 350

cgc ctg ggg aac act gaa gcc tgc tct ccg tgc cac tgc agc cct gtt   1104
Arg Leu Gly Asn Thr Glu Ala Cys Ser Pro Cys His Cys Ser Pro Val
        355                 360                 365

ggt tct ctc agc aca cag tgt gac agt tac ggc aga tgc agc tgt aag   1152
Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys Ser Cys Lys
    370                 375                 380

cca gga gtg atg ggt gac aag tgt gac cgt tgt cag cct ggg ttc cat   1200
Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro Gly Phe His
385                 390                 395                 400

tcc ctc act gag gca gga tgc agg cca tgc tcc tgc gat cct tcg ggc   1248
Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp Pro Ser Gly
                405                 410                 415

agc aca gac gag tgt aat gtt gaa aca gga aga tgc gtt tgc aaa gac   1296
Ser Thr Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val Cys Lys Asp
            420                 425                 430

aat gtt gaa ggc ttc aac tgt gag aga tgc aaa cct gga ttt ttt aat   1344
Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly Phe Phe Asn
        435                 440                 445

ctg gag tca tct aat cct aag ggc tgc aca ccc tgc ttc tgc ttt ggc   1392
Leu Glu Ser Ser Asn Pro Lys Gly Cys Thr Pro Cys Phe Cys Phe Gly
    450                 455                 460

cat tct tct gtg tgc aca aat gct gtt ggc tac agt gtt tat gac atc   1440
His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val Tyr Asp Ile
465                 470                 475                 480
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tcc tcc acc ttt cag att gat gag gat ggg tgg cgc gtg gag cag aga   1488
Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Val Glu Gln Arg
                485                 490                 495

gat ggc tcg gag gcg tct ctg gag tgg tcc tca gac agg caa tat att   1536
Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Asp Arg Gln Tyr Ile
            500                 505                 510

gcc gta atc tca gac agt tac ttt cct aga tac ttc atc gcc cct gtg   1584
Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile Ala Pro Val
        515                 520                 525

aag ttc ctg ggc aac cag gtc ctg agt tat ggg cag aat ctt tcc ttc   1632
Lys Phe Leu Gly Asn Gln Val Leu Ser Tyr Gly Gln Asn Leu Ser Phe
    530                 535                 540

tcc ttc cga gtg gac aga cga gac act cgc ctc tcc gca gag gac ctt   1680
Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala Glu Asp Leu
545                 550                 555                 560

gtg ctc gaa gga gct ggc ttg aga gta tcc gtg ccc ttg atc gct cag   1728
Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu Ile Ala Gln
                565                 570                 575

ggc aac tcc tac ccc agc gag acc act gtg aag tac atc ttc agg ctc   1776
Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Ile Phe Arg Leu
            580                 585                 590

cat gaa gca acg gat tac cct tgg agg ccc gct ctc tcc ccg ttt gaa   1824
His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Ser Pro Phe Glu
        595                 600                 605

ttt cag aag ctc ctg aac aac ttg acc tct atc aag atc cgt ggt aca   1872
Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile Arg Gly Thr
    610                 615                 620

tac agc gag agg agc gct ggg tac ttg gat gat gtc acc ttg caa agt   1920
Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr Leu Gln Ser
625                 630                 635                 640

gct cgc cct ggg ccc gga gtc cct gca acg tgg gtg gag tcc tgc acc   1968
Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu Ser Cys Thr
                645                 650                 655

tgt cca gtg gga tac ggg gga cag ttc tgt gag acg tgc ctc cca ggg   2016
Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Thr Cys Leu Pro Gly
            660                 665                 670

tac aga aga gaa act cca agc ctt gga cct tat agc ccg tgt gtg ctc   2064
Tyr Arg Arg Glu Thr Pro Ser Leu Gly Pro Tyr Ser Pro Cys Val Leu
        675                 680                 685

tgt acc tgt aat ggg cac agt gag acc tgt gac ccg gag aca ggt gtc   2112
Cys Thr Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu Thr Gly Val
    690                 695                 700

tgt gac tgc aga gac aat aca gcc ggc ccc cac tgt gag aaa tgt agc   2160
Cys Asp Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu Lys Cys Ser
705                 710                 715                 720

gat ggg tac tat ggg gac tca acc ctg ggc acc tcc tct gac tgc cag   2208
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Asp Gly Tyr Tyr Gly Asp Ser Thr Leu Gly Thr Ser Ser Asp Cys Gln
                725                 730                 735

cct tgt ccc tgc ccc ggt ggc tca agt tgt gcc att gtc cca aag aca   2256
Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Ile Val Pro Lys Thr
            740                 745                 750

aag gaa gtg gtg tgc acg cac tgt ccg act ggc act gcc ggc aag aga   2304
Lys Glu Val Val Cys Thr His Cys Pro Thr Gly Thr Ala Gly Lys Arg
        755                 760                 765

tgt gaa ctc tgt gat gac ggc tac ttt gga gac cct ctg ggc agc aat   2352
Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu Gly Ser Asn
    770                 775                 780

ggg ccc gtg aga ctg tgc cgc ccg tgc cag tgt aac gac aac ata gac   2400
Gly Pro Val Arg Leu Cys Arg Pro Cys Gln Cys Asn Asp Asn Ile Asp
785                 790                 795                 800

ccc aac gcg gtt ggc aac tgc aac cgc ctg acg ggc gag tgc ctg aag   2448
Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu Cys Leu Lys
                805                 810                 815

tgc atc tat aac acg gct ggt ttc tac tgc gac cgg tgc aag gaa ggg   2496
Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys Lys Glu Gly
            820                 825                 830

ttt ttc gga aat ccc ctg gct ccc aat cca gcc gac aaa tgc aaa gcc   2544
Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Lys Ala
        835                 840                 845

tgc gcc tgc aac tac ggg aca gtg cag caa cag agc agc tgt aac ccg   2592
Cys Ala Cys Asn Tyr Gly Thr Val Gln Gln Gln Ser Ser Cys Asn Pro
    850                 855                 860

gtg acc gga caa tgc cag tgt ctg cct cat gtg tct ggc cgc gac tgc   2640
Val Thr Gly Gln Cys Gln Cys Leu Pro His Val Ser Gly Arg Asp Cys
865                 870                 875                 880

ggt act tgt gac cct ggc tac tac aac ctg cag agc ggg caa ggc tgc   2688
Gly Thr Cys Asp Pro Gly Tyr Tyr Asn Leu Gln Ser Gly Gln Gly Cys
                885                 890                 895

gag agg tgt gac tgc cat gct ttg ggt tcc acc aat ggg cag tgt gac   2736
Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn Gly Gln Cys Asp
            900                 905                 910

atc cgc acc ggg cag tgt gag tgc cag cct ggc atc acc ggt cag cac   2784
Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile Thr Gly Gln His
        915                 920                 925

tgt gag cgc tgt gag acc aac cac ttt ggg ttt gga cct gaa ggc tgc   2832
Cys Glu Arg Cys Glu Thr Asn His Phe Gly Phe Gly Pro Glu Gly Cys
    930                 935                 940

aaa cct tgt gac tgt cac cat gaa gga tcc ctt tcg ctc cag tgt aaa   2880
Lys Pro Cys Asp Cys His His Glu Gly Ser Leu Ser Leu Gln Cys Lys
945                 950                 955                 960

gac gac ggc cgt tgt gaa tgc agg gaa ggc ttt gtg ggc aat cgc tgt   2928
Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val Gly Asn Arg Cys
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                965                 970                 975

gac cag tgt gaa gag aac tat ttc tac aat cgg tcc tgg cct ggc tgc   2976
Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser Trp Pro Gly Cys
            980                 985                 990

cag gag tgt ccg gct tgt tac cga ctt gtg aag gat aag gct gct gag   3024
Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp Lys Ala Ala Glu
        995                1000                1005

cat cga gtg aaa ctc cag gag tta gag agc ctc atc gcc aac ctt ggc   3072
His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile Ala Asn Leu Gly
   1010                1015                1020

act ggg gat gac atg gtg aca gat caa gcc ttt gag gac aga ctt aag   3120
Thr Gly Asp Asp Met Val Thr Asp Gln Ala Phe Glu Asp Arg Leu Lys
1025                1030                1035                1040

gaa gca gaa agg gag gtg aca gac ctt ctc cgt gag gct cag gaa gtc   3168
Glu Ala Glu Arg Glu Val Thr Asp Leu Leu Arg Glu Ala Gln Glu Val
                1045                1050                1055

aaa gat gta gat caa aat ctg atg gat cgc ctt cag aga gta aat agc   3216
Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln Arg Val Asn Ser
            1060                1065                1070

agc ctg cat agc caa att agc cga ctg cag aat atc cgg aat act atc   3264
Ser Leu His Ser Gln Ile Ser Arg Leu Gln Asn Ile Arg Asn Thr Ile
        1075                1080                1085

gaa gag acc ggg atc ttg gct gag cga gca cgg tcc cga gtg gag agt   3312
Glu Glu Thr Gly Ile Leu Ala Glu Arg Ala Arg Ser Arg Val Glu Ser
   1090                1095                1100

aca gag cag ctg att gag atc gcc tcc agg gag ctc gag aaa gca aaa   3360
Thr Glu Gln Leu Ile Glu Ile Ala Ser Arg Glu Leu Glu Lys Ala Lys
1105                1110                1115                1120

atg gcc gcc aat gtg tca atc act cag cca gag tct aca ggg gag cca   3408
Met Ala Ala Asn Val Ser Ile Thr Gln Pro Glu Ser Thr Gly Glu Pro
                1125                1130                1135

aac aac atg acc ctc ttg gca gaa gaa gcc cga agg ctt gca gag cgt   3456
Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Arg Leu Ala Glu Arg
            1140                1145                1150

cat aaa cag gaa gcc gat gac att gta cga gtg gca aag aca gcc aac   3504
His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala Lys Thr Ala Asn
        1155                1160                1165

gag act tca gct gag gca tat aat ctg ctt ttg agg acc ctg gca gga   3552
Glu Thr Ser Ala Glu Ala Tyr Asn Leu Leu Leu Arg Thr Leu Ala Gly
   1170                1175                1180

gaa aat caa act gcg ctg gag att gaa gaa ctt aac cgg aag tac gaa   3600
Glu Asn Gln Thr Ala Leu Glu Ile Glu Glu Leu Asn Arg Lys Tyr Glu
1185                1190                1195                1200

caa gca aag aac atc tct cag gac ctg gag aag cag gct gcc cga gtc   3648
Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln Ala Ala Arg Val
                1205                1210                1215
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cat gag gaa gcc aag cgt gca ggt gac aaa gcc gta gag atc tat gcc   3696
His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val Glu Ile Tyr Ala
          1220                1225                1230

agt gtg gcc cag ctg acc cct gtg gac tct gag gcc ctg gag aat gaa   3744
Ser Val Ala Gln Leu Thr Pro Val Asp Ser Glu Ala Leu Glu Asn Glu
       1235                1240                1245

gca aat aaa atc aag aaa gaa gct gca gac ctg gac cgt ctg att gac   3792
Ala Asn Lys Ile Lys Lys Glu Ala Ala Asp Leu Asp Arg Leu Ile Asp
   1250                1255                1260

cag aag cta aag gat tac gag gac ctc agg gaa gac atg aga gga aag   3840
Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp Met Arg Gly Lys
1265                1270                1275                1280

gaa cat gaa gtg aag aac ctt cta gag aag ggg aaa gct gaa cag cag   3888
Glu His Glu Val Lys Asn Leu Leu Glu Lys Gly Lys Ala Glu Gln Gln
              1285                1290                1295

acc gcc gac caa ctc cta gct cga gcc gat gct gcc aag gcc ctt gct   3936
Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala Lys Ala Leu Ala
          1300                1305                1310

gaa gaa gct gct aag aag gga cgc agt acc tta caa gaa gcc aat gac   3984
Glu Glu Ala Ala Lys Lys Gly Arg Ser Thr Leu Gln Glu Ala Asn Asp
       1315                1320                1325

att ctc aac aac ctg aaa gat ttt gat aga cgt gtg aac gat aac aag   4032
Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val Asn Asp Asn Lys
   1330                1335                1340

aca gcc gcg gaa gaa gct cta agg aga att ccc gcc atc aac cgg acc   4080
Thr Ala Ala Glu Glu Ala Leu Arg Arg Ile Pro Ala Ile Asn Arg Thr
1345                1350                1355                1360

ata gct gaa gcc aat gag aag aca agg gag gcc cag cta gcg ctg ggc   4128
Ile Ala Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln Leu Ala Leu Gly
              1365                1370                1375

aat gct gcc gct gac gcc acg gag gcc aag aac aag gcc cat gag gca   4176
Asn Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys Ala His Glu Ala
          1380                1385                1390

gag agg atc gcc agc gcc gcg cag aag aat gcc acc agt acc aag gcg   4224
Glu Arg Ile Ala Ser Ala Ala Gln Lys Asn Ala Thr Ser Thr Lys Ala
       1395                1400                1405

gac gca gaa aga acc ttc ggg gaa gtt aca gat ctg gat aat gag gtg   4272
Asp Ala Glu Arg Thr Phe Gly Glu Val Thr Asp Leu Asp Asn Glu Val
   1410                1415                1420

aac ggt atg ctg agg cag cta gag gag gca gag aat gag ctg aag agg   4320
Asn Gly Met Leu Arg Gln Leu Glu Glu Ala Glu Asn Glu Leu Lys Arg
1425                1430                1435                1440

aag caa gat gac gcc gac cag gac atg atg atg gcg ggg atg gct tcg   4368
Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala Gly Met Ala Ser
              1445                1450                1455
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caa gcc gct cag gag gct gag ctc aat gcc aga aag gcc aaa aac tct   4416
Gln Ala Ala Gln Glu Ala Glu Leu Asn Ala Arg Lys Ala Lys Asn Ser
          1460                1465                1470

gtc agc agc ctc ctc agc cag ctg aac aac ctc ttg gat cag cta gga   4464
Val Ser Ser Leu Leu Ser Gln Leu Asn Asn Leu Leu Asp Gln Leu Gly
       1475                1480                1485

cag ctg gac aca gtg gac ctg aac aag ctc aat gag atc gaa ggc tcc   4512
Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu Ile Glu Gly Ser
   1490                1495                1500

ctg aac aaa gcc aaa gac gaa atg aag gcc agc gac ctg gac agg aag   4560
Leu Asn Lys Ala Lys Asp Glu Met Lys Ala Ser Asp Leu Asp Arg Lys
1505                1510                1515                1520

gtg tct gac ctg gag agc gag gct cgg aag cag gaa gca gcc atc atg   4608
Val Ser Asp Leu Glu Ser Glu Ala Arg Lys Gln Glu Ala Ala Ile Met
               1525                1530                1535

gac tat aac cgg gac ata gca gag atc att aag gat att cac aac ctg   4656
Asp Tyr Asn Arg Asp Ile Ala Glu Ile Ile Lys Asp Ile His Asn Leu
          1540                1545                1550

gag gac atc aag aag acc cta cca acc ggc tgc ttc aac acc ccg tct   4704
Glu Asp Ile Lys Lys Thr Leu Pro Thr Gly Cys Phe Asn Thr Pro Ser
       1555                1560                1565

atc gag aag ccc tagtggcgag agggctgtaa ggcagtgtcc ctgacagggg       4756
Ile Glu Lys Pro
   1570

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aaaacagtat tttatttata ataaaatctg aatatttgta acccttt 7263

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<211> 1572
<212> PRT
<213> Mus musculus

<400> 32

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Thr Cys Gly Thr Pro Pro Glu Glu Tyr Cys Val Gln Thr Gly Val Thr
        35                  40                  45

Gly Val Thr Lys Ser Cys His Leu Cys Asp Ala Gly Gln Gln His Leu
    50                  55                  60

Gln His Gly Ala Ala Phe Leu Thr Asp Tyr Asn Asn Gln Ala Asp Thr
65                  70                  75                  80

Thr Trp Trp Gln Ser Gln Thr Met Leu Ala Gly Val Gln Tyr Pro Asn
                85                  90                  95

Ser Ile Asn Leu Thr Leu His Leu Gly Lys Ala Phe Asp Ile Thr Tyr
            100                 105                 110

Val Arg Leu Lys Phe His Thr Ser Arg Pro Glu Ser Phe Ala Ile Tyr
        115                 120                 125

Lys Arg Thr Arg Glu Asp Gly Pro Trp Ile Pro Tyr Gln Tyr Tyr Ser
    130                 135                 140

Gly Ser Cys Glu Asn Thr Tyr Ser Lys Ala Asn Arg Gly Phe Ile Arg
145                 150                 155                 160

Thr Gly Gly Asp Glu Gln Gln Ala Leu Cys Thr Asp Glu Phe Ser Asp
                165                 170                 175

Ile Ser Pro Leu Thr Gly Gly Asn Val Ala Phe Ser Thr Leu Glu Gly
            180                 185                 190

Arg Pro Ser Ala Tyr Asn Phe Asp Asn Ser Pro Val Leu Gln Glu Trp
        195                 200                 205

Val Thr Ala Thr Asp Ile Arg Val Thr Leu Asn Arg Leu Asn Thr Phe
    210                 215                 220

Gly Asp Glu Val Phe Asn Asp Pro Lys Val Leu Lys Ser Tyr Tyr Tyr
225                 230                 235                 240

Ala Ile Ser Asp Phe Ala Val Gly Gly Arg Cys Lys Cys Asn Gly His
                245                 250                 255

Ala Ser Glu Cys Val Lys Asn Glu Phe Asp Lys Leu Met Cys Asn Cys
            260                 265                 270

Lys His Asn Thr Tyr Gly Val Asp Cys Glu Lys Cys Leu Pro Phe Phe
        275                 280                 285

Asn Asp Arg Pro Trp Arg Arg Ala Thr Ala Glu Ser Ala Ser Glu Cys
    290                 295                 300

Leu Pro Cys Asp Cys Asn Gly Arg Ser Gln Glu Cys Tyr Phe Asp Pro
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Asp Asn Thr Asp Gly Ala Lys Cys Glu Arg Cys Arg Glu Asn Phe Phe
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Arg Leu Gly Asn Thr Glu Ala Cys Ser Pro Cys His Cys Ser Pro Val
        355                 360                 365

Gly Ser Leu Ser Thr Gln Cys Asp Ser Tyr Gly Arg Cys Ser Cys Lys
    370                 375                 380

Pro Gly Val Met Gly Asp Lys Cys Asp Arg Cys Gln Pro Gly Phe His
385                 390                 395                 400

Ser Leu Thr Glu Ala Gly Cys Arg Pro Cys Ser Cys Asp Pro Ser Gly
                405                 410                 415

Ser Thr Asp Glu Cys Asn Val Glu Thr Gly Arg Cys Val Cys Lys Asp
            420                 425                 430

Asn Val Glu Gly Phe Asn Cys Glu Arg Cys Lys Pro Gly Phe Phe Asn
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Leu Glu Ser Ser Asn Pro Lys Gly Cys Thr Pro Cys Phe Cys Phe Gly
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His Ser Ser Val Cys Thr Asn Ala Val Gly Tyr Ser Val Tyr Asp Ile
465                 470                 475                 480

Ser Ser Thr Phe Gln Ile Asp Glu Asp Gly Trp Arg Val Glu Gln Arg
                485                 490                 495

Asp Gly Ser Glu Ala Ser Leu Glu Trp Ser Ser Asp Arg Gln Tyr Ile
            500                 505                 510

Ala Val Ile Ser Asp Ser Tyr Phe Pro Arg Tyr Phe Ile Ala Pro Val
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Lys Phe Leu Gly Asn Gln Val Leu Ser Tyr Gly Gln Asn Leu Ser Phe
    530                 535                 540

Ser Phe Arg Val Asp Arg Arg Asp Thr Arg Leu Ser Ala Glu Asp Leu
545                 550                 555                 560

Val Leu Glu Gly Ala Gly Leu Arg Val Ser Val Pro Leu Ile Ala Gln
                565                 570                 575

Gly Asn Ser Tyr Pro Ser Glu Thr Thr Val Lys Tyr Ile Phe Arg Leu
            580                 585                 590

His Glu Ala Thr Asp Tyr Pro Trp Arg Pro Ala Leu Ser Pro Phe Glu
        595                 600                 605

Phe Gln Lys Leu Leu Asn Asn Leu Thr Ser Ile Lys Ile Arg Gly Thr
    610                 615                 620

Tyr Ser Glu Arg Ser Ala Gly Tyr Leu Asp Asp Val Thr Leu Gln Ser
625                 630                 635                 640

Ala Arg Pro Gly Pro Gly Val Pro Ala Thr Trp Val Glu Ser Cys Thr
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645 650 655

Cys Pro Val Gly Tyr Gly Gly Gln Phe Cys Glu Thr Cys Leu Pro Gly
660 665 670

Tyr Arg Arg Glu Thr Pro Ser Leu Gly Pro Tyr Ser Pro Cys Val Leu
675 680 685

Cys Thr Cys Asn Gly His Ser Glu Thr Cys Asp Pro Glu Thr Gly Val
690 695 700

Cys Asp Cys Arg Asp Asn Thr Ala Gly Pro His Cys Glu Lys Cys Ser
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Asp Gly Tyr Tyr Gly Asp Ser Thr Leu Gly Thr Ser Ser Asp Cys Gln
725 730 735

Pro Cys Pro Cys Pro Gly Gly Ser Ser Cys Ala Ile Val Pro Lys Thr
740 745 750

Lys Glu Val Val Cys Thr His Cys Pro Thr Gly Thr Ala Gly Lys Arg
755 760 765

Cys Glu Leu Cys Asp Asp Gly Tyr Phe Gly Asp Pro Leu Gly Ser Asn
770 775 780

Gly Pro Val Arg Leu Cys Arg Pro Cys Gln Cys Asn Asp Asn Ile Asp
785 790 795 800

Pro Asn Ala Val Gly Asn Cys Asn Arg Leu Thr Gly Glu Cys Leu Lys
805 810 815

Cys Ile Tyr Asn Thr Ala Gly Phe Tyr Cys Asp Arg Cys Lys Glu Gly
820 825 830

Phe Phe Gly Asn Pro Leu Ala Pro Asn Pro Ala Asp Lys Cys Lys Ala
835 840 845

Cys Ala Cys Asn Tyr Gly Thr Val Gln Gln Gln Ser Ser Cys Asn Pro
850 855 860

Val Thr Gly Gln Cys Gln Cys Leu Pro His Val Ser Gly Arg Asp Cys
865 870 875 880

Gly Thr Cys Asp Pro Gly Tyr Tyr Asn Leu Gln Ser Gly Gln Gly Cys
885 890 895

Glu Arg Cys Asp Cys His Ala Leu Gly Ser Thr Asn Gly Gln Cys Asp
900 905 910

Ile Arg Thr Gly Gln Cys Glu Cys Gln Pro Gly Ile Thr Gly Gln His
915 920 925

Cys Glu Arg Cys Glu Thr Asn His Phe Gly Phe Gly Pro Glu Gly Cys
930 935 940

Lys Pro Cys Asp Cys His His Glu Gly Ser Leu Ser Leu Gln Cys Lys
945 950 955 960

Asp Asp Gly Arg Cys Glu Cys Arg Glu Gly Phe Val Gly Asn Arg Cys
965 970 975

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Asp Gln Cys Glu Glu Asn Tyr Phe Tyr Asn Arg Ser Trp Pro Gly Cys
            980                 985                 990

Gln Glu Cys Pro Ala Cys Tyr Arg Leu Val Lys Asp Lys Ala Ala Glu
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His Arg Val Lys Leu Gln Glu Leu Glu Ser Leu Ile Ala Asn Leu Gly
   1010                1015                1020

Thr Gly Asp Asp Met Val Thr Asp Gln Ala Phe Glu Asp Arg Leu Lys
1025                1030                1035                1040

Glu Ala Glu Arg Glu Val Thr Asp Leu Leu Arg Glu Ala Gln Glu Val
                1045                1050                1055

Lys Asp Val Asp Gln Asn Leu Met Asp Arg Leu Gln Arg Val Asn Ser
           1060                1065                1070

Ser Leu His Ser Gln Ile Ser Arg Leu Gln Asn Ile Arg Asn Thr Ile
       1075                1080                1085

Glu Glu Thr Gly Ile Leu Ala Glu Arg Ala Arg Ser Arg Val Glu Ser
   1090                1095                1100

Thr Glu Gln Leu Ile Glu Ile Ala Ser Arg Glu Leu Glu Lys Ala Lys
1105                1110                1115                1120

Met Ala Ala Asn Val Ser Ile Thr Gln Pro Glu Ser Thr Gly Glu Pro
                1125                1130                1135

Asn Asn Met Thr Leu Leu Ala Glu Glu Ala Arg Arg Leu Ala Glu Arg
           1140                1145                1150

His Lys Gln Glu Ala Asp Asp Ile Val Arg Val Ala Lys Thr Ala Asn
       1155                1160                1165

Glu Thr Ser Ala Glu Ala Tyr Asn Leu Leu Leu Arg Thr Leu Ala Gly
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Glu Asn Gln Thr Ala Leu Glu Ile Glu Glu Leu Asn Arg Lys Tyr Glu
1185                1190                1195                1200

Gln Ala Lys Asn Ile Ser Gln Asp Leu Glu Lys Gln Ala Ala Arg Val
                1205                1210                1215

His Glu Glu Ala Lys Arg Ala Gly Asp Lys Ala Val Glu Ile Tyr Ala
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Ser Val Ala Gln Leu Thr Pro Val Asp Ser Glu Ala Leu Glu Asn Glu
       1235                1240                1245

Ala Asn Lys Ile Lys Lys Glu Ala Ala Asp Leu Asp Arg Leu Ile Asp
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Gln Lys Leu Lys Asp Tyr Glu Asp Leu Arg Glu Asp Met Arg Gly Lys
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Glu His Glu Val Lys Asn Leu Leu Glu Lys Gly Lys Ala Glu Gln Gln
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Thr Ala Asp Gln Leu Leu Ala Arg Ala Asp Ala Ala Lys Ala Leu Ala
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Glu Glu Ala Ala Lys Lys Gly Arg Ser Thr Leu Gln Glu Ala Asn Asp
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Ile Leu Asn Asn Leu Lys Asp Phe Asp Arg Arg Val Asn Asp Asn Lys
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Thr Ala Ala Glu Glu Ala Leu Arg Arg Ile Pro Ala Ile Asn Arg Thr
1345                1350                1355                1360

Ile Ala Glu Ala Asn Glu Lys Thr Arg Glu Ala Gln Leu Ala Leu Gly
               1365                1370                1375

Asn Ala Ala Ala Asp Ala Thr Glu Ala Lys Asn Lys Ala His Glu Ala
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Glu Arg Ile Ala Ser Ala Ala Gln Lys Asn Ala Thr Ser Thr Lys Ala
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Asp Ala Glu Arg Thr Phe Gly Glu Val Thr Asp Leu Asp Asn Glu Val
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Asn Gly Met Leu Arg Gln Leu Glu Glu Ala Glu Asn Glu Leu Lys Arg
1425                1430                1435                1440

Lys Gln Asp Asp Ala Asp Gln Asp Met Met Met Ala Gly Met Ala Ser
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Val Ser Ser Leu Leu Ser Gln Leu Asn Asn Leu Leu Asp Gln Leu Gly
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Gln Leu Asp Thr Val Asp Leu Asn Lys Leu Asn Glu Ile Glu Gly Ser
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Ile Glu Lys Pro
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(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
9 November 2000 (09.11.2000)

PCT

(10) International Publication Number
WO 00/66730 A3

(51) International Patent Classification[7]: C12N 15/12, 15/62, 5/10, C07K 14/78, A61K 38/39, A61P 9/00, 21/00, 25/00, A61L 31/00

(21) International Application Number: PCT/US00/11378

(22) International Filing Date: 28 April 2000 (28.04.2000)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/131,720	30 April 1999 (30.04.1999)	US
60/139,198	15 June 1999 (15.06.1999)	US
60/143,289	12 July 1999 (12.07.1999)	US
60/155,945	24 September 1999 (24.09.1999)	US

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(75) Inventor/Applicant *(for US only)*: YURCHENCO, Peter [US/US]; University of Medicine and Dentistry of New Jersey Robert Wood Johnson Medical School, 675 Hoes Lane, Piscataway, NJ 08854-5635 (US).

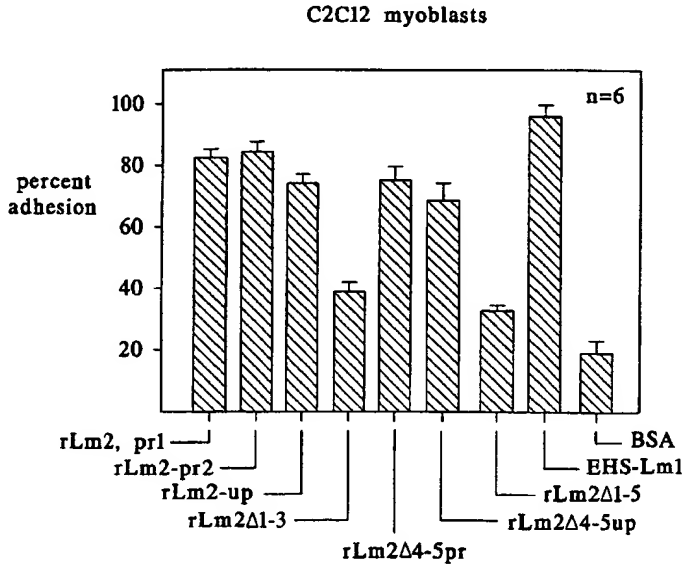
(74) Agent: HARPER, David, S.; McDonnell, Boehnen, Hulbert & Berghoff, Suite 3200, 300 South Wacker Drive, Chicago, IL 60606 (US).

(81) Designated States *(national)*: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: LAMININ 2 AND METHODS FOR ITS USE



(57) Abstract: The present invention provides substantially purified laminin 2, methods for making recombinant laminin 2, cells that express recombinant laminin 2, and methods for using the substantially purified laminin 2 to accelerate peripheral nervous system nerve regeneration, and to promote cell attachment and migration.

WO 00/66730 A3

Published:
— *With international search report.*

(88) Date of publication of the international search report:
19 April 2001

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

INTERNATIONAL SEARCH REPORT

Intern al Application No
PCT/US 00/11378

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/12 C12N15/62 C12N5/10 C07K14/78 A61K38/39
A61P9/00 A61P21/00 A61P25/00 A61L31/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 08628 A (JOLLA CANCER RES FOUND) 30 March 1995 (1995-03-30)	30-33
Y	SeqIdNo.4: 100.0% identity in 3098 aa overlap with SeqIdNo.2 / 99.8% identity in 9535nt overlap with SeqIdNo.1 claims 14-16,18,30,33; figure 6	16-18, 22-24, 28,29
X	UTANI A ET AL: "A specific sequence of the laminin alpha 2 chain critical for the initiation of heterotrimer assembly" JOURNAL OF BIOLOGICAL CHEMISTRY., vol. 270, no. 7, 17 February 1995 (1995-02-17), pages 3292-3298, XP002153607	1-15
Y	figure 4	16-18, 22-24, 28,29

-/--

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
8 December 2000	22/12/2000

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Lonnoy, O

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	TALTS J ET AL: "Structural analysis and proteolytic processing of recombinant G domain of mouse laminin alpha2 chain" FEBS LETTERS., vol. 426, no. 1, 10 April 1998 (1998-04-10), pages 71-76, XP002153608 figure 1B	30-33
Y	DATABASE EMEST EBI, Hinxton, U.K.; Accession Number: AA028205, 17 August 1996 (1996-08-17) HILLIER L ET AL: "Homo sapiens cDNA clone IMAGE:364820 5' similar to gb:Z26653 MEROSIN HEAVY CHAIN (HUMAN)" XP002153610 abstract	30-33
A	WO 92 12727 A (UNIV MINNESOTA) 6 August 1992 (1992-08-06)	
A	WO 95 09012 A (JOLLA CANCER RES FOUND ;ARAHATA KIICHI (JP)) 6 April 1995 (1995-04-06)	
A	VACHON P ET AL: "Merosin and laminin in myogenesis; specific requirement for merosin in myotube stability and survival" J CELL BIOL, vol. 134, no. 6, September 1996 (1996-09), pages 1483-1497, XP002153609 cited in the application	

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-29 (all totally) and 34 (partially)

   Laminin 2, materials and methods for its recombinant production, and applications thereof.

2. Claims: 30-33 (all totally) and 34 (partially)

   Laminin alpha 2 chain consisting of the sequence SeqIdNo.1-2, and application thereof.

INTERNATIONAL SEARCH REPORT

mation on patent family members

Internal Application No
PCT/US 00/11378

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9508628 A	30-03-1995	US 5872231 A	16-02-1999
		AU 7877094 A	10-04-1995
		CA 2172385 A	30-03-1995
		EP 0720651 A	10-07-1996
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WO 9509012 A	06-04-1995	US 5780244 A	14-07-1998